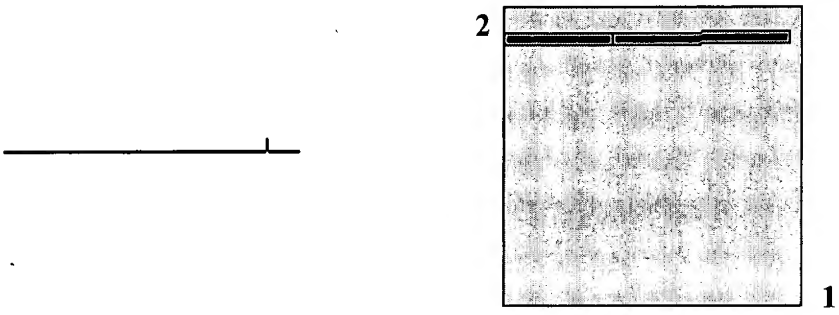
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.0 wordsize: 11 Filter ☑ Align

Sequence 1 lcl|seq_1 **Length** 22 (1 .. 22)

Sequence 2 gi 3006202 Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds. **Length** 3901 (1 .. 3901)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 29.5 bits (15), Expect = 5.6
Identities = 22/23 (95%), Gaps = 1/23 (4%)
 Strand = Plus / Plus

Query: 1    cctccaatt-ccccttaaactt 22
            ||||||||| ||||||||||||
Sbjct: 3465 cctccaattccccccttaaactt 3487

CPU time:     0.02 user secs.       0.04 sys. secs          0.06 total secs.

Gapped
Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 3
Number of Sequences: 0
Number of extensions: 3
Number of successful extensions: 3
Number of sequences better than 10.0: 1
```

```
length of query: 22
length of database: 4,611,916,737
effective HSP length: 21
effective length of query: 1
effective length of database: 4,309,374,105
effective search space: 4309374105
effective search space used: 4309374105
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 15 (29.5 bits)
```

☐ 1: U46768. Human stanniocalc...[gi:1199619] Related Sequences, OMIM, Protein, Taxonomy, LinkOut

```
LOCUS       HSU46768                 840 bp    mRNA    linear   PRI 22-FEB-1996
DEFINITION  Human stanniocalcin mRNA, complete cds.
ACCESSION   U46768
VERSION     U46768.1  GI:1199619
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   Olsen,H.S., Cepeda,M.A., Zhang,Q.-Q., Rosen,C.A., Vozzolo,B.L. and
            Wagner,G.F.
  TITLE     Human stanniocalcin: a hormonal regulator of mineral metabolism
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (1996) In press
REFERENCE   2  (bases 1 to 840)
  AUTHORS   Olsen,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-1996) Henrik S. Olsen, Human Genome Sciences,
            9410 Key West Avenue, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1..840
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             35..778
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAA88903.1"
                     /db_xref="GI:1199620"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEEDSPSHIKRTSHESA"
BASE COUNT      237 a    233 c    201 g    169 t
ORIGIN
        1 aaaacccaac aacttagcgg aaacttctca gagaatgctc caaaactcag cagtgcttct
       61 ggtgctggtg atcagtgctt ctgcaaccca tgaggcggag cagaatgact ctgtgagccc
      121 caggaaatcc cgagtggcgg cccaaaactc agctgaagtg gttcgttgcc tcaacagtgc
      181 tctacaggtc ggctgcgggg cttttgcatg cctggaaaac tccacctgtg acacagatgg
      241 gatgtatgac atctgtaaat ccttcttgta cagcgctgct aaatttgaca ctcagggaaa
      301 agcattcgtc aaagagagct taaaatgcat cgccaacggg gtcacctcca aggtcttcct
      361 cgccattcgg aggtgctcca ctttccaaag gatgattgct gaggtgcagg aagagtgcta
      421 cagcaagctg aatgtgtgca gcatcgccaa gcggaaccct gaagccatca ctgaggtcgt
      481 ccagctgccc aatcacttct ccaacagata ctataacaga cttgtccgaa gcctgctgga
      541 atgtgatgaa gacacagtca gcacaatcag agacagcctg atggagaaaa ttgggcctaa
      601 catggccagc ctcttccaca tcctgcagac agaccactgt gcccaaacac acccacgagc
      661 tgacttcaac aggagacgca ccaatgagcc gcagaagctg aaagtcctcc tcaggaacct
      721 ccgaggtgag gaggactctc cctcccacat caaacgcaca tcccatgaga gtgcataacc
      781 agggagaggt tattcacaac ctcaccaaac tagtatcatt ttaggggtgt tgacacacca
//
```

Revised: October 24, 2001.

```
>gi|16162450|ref|XM_011704.4| Homo sapiens stanniocalcin 1 (STC1), mRNA
          Length = 3877

 Score = 40.1 bits (20), Expect = 0.011
 Identities = 20/20 (100%)
 Strand = Plus / Minus


Query: 1    tctaggtcagcccccgaatc 20
             ||||||||||||||||||||
Sbjct: 3536 tctaggtcagcccccgaatc 3517

>gi|4507264|ref|NM_003155.1| Homo sapiens stanniocalcin 1 (STC1), mRNA
          Length = 3901

 Score = 40.1 bits (20), Expect = 0.011
 Identities = 20/20 (100%)
 Strand = Plus / Minus


Query: 1    tctaggtcagcccccgaatc 20
             ||||||||||||||||||||
Sbjct: 3538 tctaggtcagcccccgaatc 3519

>gi|6716576|gb|AF178116.1|AF178116 Canis familiaris STC1 gene, complete sequence
          Length = 1053

 Score = 40.1 bits (20), Expect = 0.011
 Identities = 20/20 (100%)
 Strand = Plus / Plus


Query: 1   tctaggtcagcccccgaatc 20
            ||||||||||||||||||||
Sbjct: 343 tctaggtcagcccccgaatc 362

>gi|3006202|gb|U25997.1|HSU25997 Homo sapiens stanniocalcin precursor (STC) mRNA,
complete cds
          Length = 3901

 Score = 40.1 bits (20), Expect = 0.011
 Identities = 20/20 (100%)
 Strand = Plus / Minus


Query: 1    tctaggtcagcccccgaatc 20
             ||||||||||||||||||||
Sbjct: 3538 tctaggtcagcccccgaatc 3519

>gi|261373|gb|S50179.1|S50179 {clone S1} [human, 76N, mammary epithelial cells, mRNA,
607 nt]
```

```
          Length = 607

 Score = 40.1 bits (20), Expect = 0.011
 Identities = 20/20 (100%)
 Strand = Plus / Minus


Query: 1   tctaggtcagcccccgaatc 20
           ||||||||||||||||||||
Sbjct: 244 tctaggtcagcccccgaatc 225
```

NCBI formatting **BLAST**

Nucleotide Protein Translations Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (20 letters)

The request ID is 1011565227-13623-17781

Format! or Reset all

The results are estimated to be ready in 2 minutes 10 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Limit results by entrez query or select from: (none)

Expect value range:

NCBI *formatting* **BLAST**

Nucleotide Protein Translations Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (22 letters)

The request ID is 1011565321-14215-1755

Format! or Reset all

The results are estimated to be ready in 2 minutes 10 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Limit results by entrez query or select from: (none)

Expect value range:

NCBI

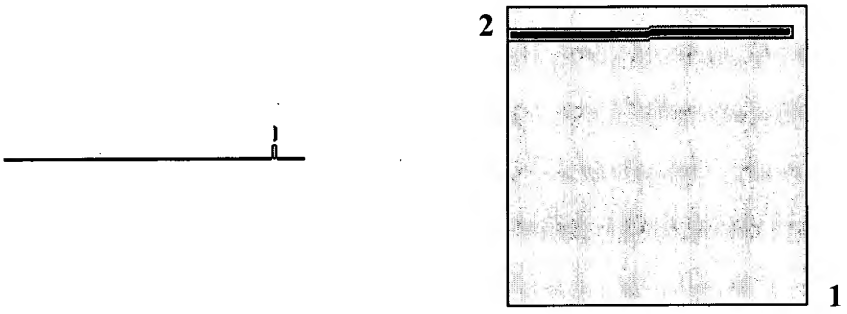
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.0 wordsize: 11 Filter ☑ Align

Sequence 1 lcl|seq_1 **Length** 20 (1 .. 20)

Sequence 2 gi 3006202 Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds. **Length** 3901 (1 .. 3901)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 39.1 bits (20), Expect = 0.007
Identities = 20/20 (100%)
 Strand = Plus / Plus
```

```
Query: 1    gattcgggggctgacctaga 20
            ||||||||||||||||||||
Sbjct: 3519 gattcgggggctgacctaga 3538

CPU time:     0.03 user secs.       0.05 sys. secs          0.08 total secs.

Gapped
Lambda      K       H
    1.33     0.621      1.12

Gapped
Lambda      K       H
    1.33     0.621      1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
```

```
length of query: 20
length of database: 4,611,916,737
effective HSP length: 19
effective length of query: 1
effective length of database: 4,310,814,769
effective search space: 4310814769
effective search space used: 4310814769
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 15 (29.5 bits)
```

```
Query: 501 ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 501 ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 560


Query: 561 aataaagtgttacgttttattggtttc 587
           |||||||||||||||||||||||||||
Sbjct: 561 aataaagtgttacgttttattggtttc 587

>gi|4507264|ref|NM_003155.1| Homo sapiens stanniocalcin 1 (STC1), mRNA
          Length = 3901

 Score = 1067 bits (538), Expect = 0.0
 Identities = 559/567 (98%), Gaps = 1/567 (0%)
 Strand = Plus / Plus


Query: 21   ggctgtgacctcttcaaaccgtggtannnnnnnttttctccccacgatgatatctatata 80
           |||||||||||||||||||||||||       |||||||||||||||||||||||||||
Sbjct: 3316 ggctgtgacctcttcaaaccgtggtacccccccttttctccccacgatgatatctatata 3375


Query: 81   tgtatctacaatacatatatctacacatacagaaagaagcagttctcacaatgttgctag 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 3376 tgtatctacaatacatatatctacacatacagaaagaagcagttctcaca-tgttgctag 3434


Query: 141  ttttttgcttctctttcccccaccctactccctccaattcccccctaaacttccaaagc 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3435 ttttttgcttctctttcccccaccctactccctccaattcccccctaaacttccaaagc 3494


Query: 201  ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3495 ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 3554


Query: 261  ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3555 ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 3614


Query: 321  ttataatttaaatgatatttaggtttttggctgagtactggaataaacagtgagcatatc 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3615 ttataatttaaatgatatttaggtttttggctgagtactggaataaacagtgagcatatc 3674


Query: 381  tggtatatgtcattatttattgttaaattacatttttaagctccatgtgcatataaagg 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3675 tggtatatgtcattatttattgttaaattacatttttaagctccatgtgcatataaagg 3734
```

Alignments

>gi|261373|gb|S50179.1|S50179 {clone S1} [human, 76N, mammary epithelial cells, mRNA, 607 nt]

Length = 607

Score = 1082 bits (546), Expect = 0.0
Identities = 560/567 (98%)
Strand = Plus / Plus

```
Query: 21  ggctgtgacctcttcaaaccgtggtannnnnnnttttctccccacgatgatatctatata 80
           ||||||||||||||||||||||||||       ||||||||||||||||||||||||||||
Sbjct: 21  ggctgtgacctcttcaaaccgtggtacccccccttttctccccacgatgatatctatata 80


Query: 81  tgtatctacaatacatatatctacacatacagaaagaagcagttctcacaatgttgctag 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 81  tgtatctacaatacatatatctacacatacagaaagaagcagttctcacaatgttgctag 140


Query: 141 ttttttgcttctctttcccccaccctactccctccaattcccccctttaaacttccaaagc 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 141 ttttttgcttctctttcccccaccctactccctccaattcccccctttaaacttccaaagc 200


Query: 201 ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 201 ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 260


Query: 261 ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 261 ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 320


Query: 321 ttataatttaaatgatatttaggtttttggctgagtactggaataaacagtgagcatatc 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 321 ttataatttaaatgatatttaggtttttggctgagtactggaataaacagtgagcatatc 380


Query: 381 tggtatatgtcattatttattgttaaattacatttttttaagctccatgtgcatataaagg 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 381 tggtatatgtcattatttattgttaaattacatttttttaagctccatgtgcatataaagg 440


Query: 441 ttatgaaacatatcatggtaatgacagatgcaagttattttatttgcttatttttttataa 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 441 ttatgaaacatatcatggtaatgacagatgcaagttattttatttgcttatttttttataa 500
```

```
Query: 441  ttatgaaacatatcatggtaatgacagatgcaagttattttatttgcttatttttttataa 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3735 ttatgaaacatatcatggtaatgacagatgcaagttattttatttgcttatttttttataa 3794


Query: 501  ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3795 ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 3854


Query: 561  aataaagtgttacgttttattggtttc 587
            |||||||||||||||||||||||||||
Sbjct: 3855 aataaagtgttacgttttattggtttc 3881
```

>gi|3006202|gb|U25997.1|HSU25997 Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds

Length = 3901

Score = 1067 bits (538), Expect = 0.0
Identities = 559/567 (98%), Gaps = 1/567 (0%)
Strand = Plus / Plus

```
Query: 21   ggctgtgacctcttcaaaccgtggtannnnnnnttttctccccacgatgatatctatata 80
            |||||||||||||||||||||||||       |||||||||||||||||||||||||||
Sbjct: 3316 ggctgtgacctcttcaaaccgtggtacccccccttttctccccacgatgatatctatata 3375


Query: 81   tgtatctacaatacatatatctacacatacagaaagaagcagttctcacaatgttgctag 140
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct: 3376 tgtatctacaatacatatatctacacatacagaaagaagcagttctcaca-tgttgctag 3434


Query: 141  ttttttgcttctctttcccccaccctactccctccaattcccccctttaaacttccaaagc 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3435 ttttttgcttctctttcccccaccctactccctccaattcccccctttaaacttccaaagc 3494


Query: 201  ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3495 ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 3554


Query: 261  ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3555 ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 3614


Query: 321  ttataatttaaatgatatttaggttttggctgagtactggaataaacagtgagcatatc 380
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3615 ttataatttaaatgatatttaggtttttggctgagtactggaataaacagtgagcatatc 3674


Query: 381  tggtatatgtcattatttattgttaaattacatttttttaagctccatgtgcatataaagg 440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3675 tggtatatgtcattatttattgttaaattacatttttttaagctccatgtgcatataaagg 3734


Query: 441  ttatgaaacatatcatggtaatgacagatgcaagttatttttatttgcttatttttttataa 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3735 ttatgaaacatatcatggtaatgacagatgcaagttatttttatttgcttatttttttataa 3794


Query: 501  ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3795 ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 3854


Query: 561  aataaagtgttacgttttattggtttc 587
            |||||||||||||||||||||||||||
Sbjct: 3855 aataaagtgttacgttttattggtttc 3881

>gi|16162450|ref|XM_011704.4| Homo sapiens stanniocalcin 1 (STC1), mRNA
          Length = 3877

 Score = 1035 bits (522), Expect = 0.0
 Identities = 557/567 (98%), Gaps = 3/567 (0%)
 Strand = Plus / Plus


Query: 21   ggctgtgacctcttcaaaccgtggtannnnnnnttttctccccacgatgatatctatata 80
            |||||||||||||||||||||||||       ||||||||||||||||||||||||||||
Sbjct: 3314 ggctgtgacctcttcaaaccgtggtacccccccttttctccccacgatgatatctatata 3373


Query: 81   tgtatctacaatacatatatctacacatacagaaagaagcagttctcacaatgttgctag 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3374 tgtatctacaatacatatatctacacatacagaaagaagcagttctcacaatgttgctag 3433


Query: 141  ttttttgcttctctttcccccaccctactccctccaattcccccctttaaacttccaaagc 200
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct: 3434 ttttttgcttctctttcccccaccctactccctccaattccccc-ttaaacttccaaagc 3492


Query: 201  ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3493 ttcgtcttgtgtttgctgcagagtgattcgggggctgacctagaccagtttgcatgattc 3552
```

```
Query: 261  ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3553 ttctcttgtgatttggttgcactttagacatttttgtgccattatatttgcattatgtat 3612


Query: 321  ttataatttaaatgatatttaggtttttggctgagtactggaataaacagtgagcatatc 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3613 ttataatttaaatgatatttaggtttttggctgagtactggaataaacagtgagcatatc 3672


Query: 381  tggtatatgtcattatttattgttaaattacatttttaagctccatgtgcatataaagg 440
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct: 3673 tggtatatgtcattatttattgttaaattaca-tttttaagctccatgtgcatataaagg 3731


Query: 441  ttatgaaacatatcatggtaatgacagatgcaagttattttatttgcttatttttataa 500
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 3732 ttatgaaacatatcatggtaatgacagatgcaagttattttatttgctta-tttttataa 3790


Query: 501  ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3791 ttaaagatgccatagcataatatgaagcctttggtgaattccttctaagataaaaataat 3850


Query: 561  aataaagtgttacgttttattggtttc 587
            |||||||||||||||||||||||||||
Sbjct: 3851 aataaagtgttacgttttattggtttc 3877
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     (FILE 'HOME' ENTERED AT 15:45:20 ON 20 JAN 2002)

     FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
15:45:52
     ON 20 JAN 2002
L1           703 S STANNIOCALCIN OR STANNIUS
L2            35 S L1 AND (MESOTHELIOMA# OR CANCER# OR TUMOR# OR TUMOUR# OR
CARC
L3            18 S L2 AND PY<2000
L4            16 S L1 AND (MALIGNAN? OR METASTA? OR NEOPLAS?)
L5             5 S L4 AND PY<2000
L6            18 S L3 OR L5
L7             9 DUP REM L6 (9 DUPLICATES REMOVED)

     FILE 'REGISTRY' ENTERED AT 16:03:34 ON 20 JAN 2002
L8            44 S STANNIOCALCIN

     FILE 'CAPLUS' ENTERED AT 16:10:06 ON 20 JAN 2002
L9           139 S L8
L10           19 S L9 AND (TUMOR# OR TUMOUR# OR CANCER# OR MALIGNAN? OR NEOPLAS

     FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
16:31:03
     ON 20 JAN 2002
L11            0 S L1 AND (LEUKEMIA# OR LEUKAEMIA# OR LEUKEAMIA# OR LYMPHOMA#
OR

     FILE 'JAPIO' ENTERED AT 16:47:13 ON 20 JAN 2002
L12            5 S STANNIOCALCIN

     FILE 'SCISEARCH' ENTERED AT 16:52:08 ON 20 JAN 2002
L13         1762 S REDDEL?/RAU
L14            0 S L13(S)3/RVL(S)299/RPG
L15            4 S L13(S)1996/RPY

     FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
16:56:47
     ON 20 JAN 2002
L16           20 S L1 AND REDDEL?/AU
L17           20 S L1 AND CHANG?/AU
L18           20 S L16 OR L17
L19           15 S L18 AND PY<2000
L20            6 DUP REM L19 (9 DUPLICATES REMOVED)
L21           25 S LNG108 OR LUNG108 OR (LNG(A)108) OR (LUNG(A)108)
L22           11 DUP REM L21 (14 DUPLICATES REMOVED)

=>
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DB Name	Query	Hit Count	Set Name
JPAB,EPAB,DWPI	l13 and (leukemia$1 or leukaemia$1 or leukeamia$1 or lymphoma$1 or myeloma$1)	2	L14
JPAB,EPAB,DWPI	stanniocalcin or stannius	23	L13
USPT	l10 and @prad<19991104	0	L12
USPT	l10 and @ad<19991104	3	L11
USPT	l9 and (leukemia$1 or leukaemia$1 or leukeamia$1 or lymphoma$1 or myeloma$1)	4	L10
USPT	stanniocalcin or stannius	8	L9
USPT	l7 or l6	37	L8
USPT	l5 and @prad<19991104	2	L7
USPT	l5 and @ad<19991104	37	L6
USPT	l3 not l4	38	L5
USPT	l2 same (leukemia$1 or leukaemia$1 or leukeamia$1 or lymphoma$1 or myeloma$1)	3	L4
USPT	l2 and (leukemia$1 or leukaemia$1 or leukeamia$1 or lymphoma$1 or myeloma$1)	41	L3
USPT	stc$1 or stanniocalcin or stannius	2799	L2
USPT	stc$1 or stanniocalcin or stannius	2799	L1

DB Name	Query	Hit Count	Set Name
USPT	l12 and 1426	1	L19
USPT	l12 and (SEQ ID NO: 1426)	0	L18
USPT	l12 and (SEQ ID NO:1426)	0	L17
USPT	l14 and l11	0	L16
USPT	l14 and l10	0	L15
USPT	prostate cancer antigen$1	10	L14
USPT	l10 and l11	5	L13
USPT	l10 or l11	78	L12
USPT	l8 and ruben$10[in]	15	L11
USPT	l8 and rosen$10[in]	68	L10
USPT	l8 and rosen$[in]	68	L9
USPT	prostate	8488	L8
USPT	rosen$[in]	5313	L7
USPT	l4 and @prad<19991104	0	L6
USPT	l4 and @ad<19991104	7	L5
USPT	l3 and (cancer$1 or tumor$1 or tumour$1 or mesothelioma$1 or carcinoma$1 or adenocarcinoma$1 or malignan$4)	8	L4
USPT	l1 or l2	8	L3
USPT	stanniocalcin	8	L2
USPT	stannius adj2 protein$1	4	L1

L21 ANSWER 1 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1999:476721 SCISEARCH
THE GENUINE ARTICLE: 206MU
TITLE: Preliminary studies on tin miners' lung **cancer** tissue related genes by differential display **mRNA**
AUTHOR: Yang M Y (Reprint); Ye C Q; Yao S X; Zhang J; Chen J Y; Liu L H
CORPORATE SOURCE: INST RADIAT MED, BEIJING 100850, PEOPLES R CHINA (Reprint); CHINA NATL NONFERROUS MET IND CORP, YUNNAN TIN CORP, INST LABOR PROTECT, GEJIU 661400, PEOPLES R CHINA
COUNTRY OF AUTHOR: PEOPLES R CHINA
SOURCE: CHINESE MEDICAL JOURNAL, (**JUN 1999**) Vol. 112, No. 6, pp. 529-533.
Publisher: CHINESE MEDICAL ASSOCIATION, 42 DONGSI XIDAJIE,
BEIJING 100710, PEOPLES R CHINA.
ISSN: 0366-6999.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: CLIN
LANGUAGE: English
REFERENCE COUNT: 13

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Objective To study the genes related to tin miners' lung cancer tissue.

Method Differential display mRNA.

Results Thirty cDNA fragments which differentially expressed in lung cancer tissues and the same patient's normal lung tissues were discovered.

Among these, 16 expressed in lung cancer tissues, not in normal lung tissues; fourteen expressed on the contrary. Six cDNA fragment sequence was determined. Five sequences CG2, CG7, CG8, CA5 and CC6 had less than 75% homology with known sequences in GenBank BLAST, so they were believed to be new sequences which we have recorded in Genbank. Only one fragment coded CG3 had homology up to 95% with human ribosome protein L27a gene.

Conclusions mRNA differential display provides a unique and powerful experimental system to study differential gene expression in tin miners' lung cancer tissues and the same patient's normal lung tissues. Using the system, differential expression of 30 cDNA fragments was observed. Six of them may be used to study the molecular mechanism of miners' radon-associated lung cancer.

L21 ANSWER 2 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1999:310928 SCISEARCH
THE GENUINE ARTICLE: 187GQ
TITLE: Reduced expression of the CXCR4 receptor **mRNA** in hepatocellular **carcinoma** and lack of inducibility of its ligand alpha-chemokine hIRH/SDF1 alpha/PBSF in vitro
AUTHOR: Begum N A; Shibuta K; Mori M; Barnard G F (Reprint)
CORPORATE SOURCE: UNIV MASSACHUSETTS, MED CTR, DIV DIGEST DIS & NUTR S6 737,
55 LAKE AVE N, WORCESTER, MA 01655 (Reprint); UNIV MASSACHUSETTS, MED CTR, DEPT MED, WORCESTER, MA 01655; UNIV MASSACHUSETTS, MED CTR, DEPT BIOCHEM, WORCESTER, MA 01655; UNIV MASSACHUSETTS, MED CTR, DEPT MOL BIOL, WORCESTER, MA 01655; KYUSHU UNIV, MED INST BIOREGULAT, DEPT SURG, BEPPU, OITA, JAPAN

COUNTRY OF AUTHOR: USA; JAPAN
SOURCE: INTERNATIONAL JOURNAL OF ONCOLOGY, (**MAY 1999**)
Vol. 14, No. 5, pp. 927-934.
Publisher: PROFESSOR D A SPANDIDOS, 1, S MERKOURI ST, EDITORIAL OFFICE, ATHENS 116 35, GREECE.
ISSN: 1019-6439.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 51

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Differential cDNA displays between hepatocellular carcinoma and adjacent non-malignant tissues have previously detected a PCR product, hIRH (human intercrine reduced in hepatomas), equivalent to SDF1 alpha/PBSF whose mRNA was lost from human hepatocellular carcinoma and other malignant and pre-malignant samples and malignant cell lines. There are no reports to date of the mRNA status of the receptor for hIRH/SDF1 alpha/PBSF, CXCR4 in malignant tissues. We report here that there is a reduction in the mRNA expression of CXCR4 in hepatocellular carcinoma as estimated by Northern blot and RT-PCR and compared to the adjacent non-malignant tissue. The average (mean +/- SD) tumor/normal ratio for CXCR4 mRNA expression, determined by RT-PCR, was 0.65+/-0.36 in 10 pairs of hepatocellular carcinomas. There was no consistent loss of CXCR4 mRNA expression in a range of malignant cell lines. The 3'-non-coding region of hIRH, had typical early response gene clement sequences. Despite the presence of these 3'-elements there was no induction of hIRH gene expression in human lung carcinoma A549 cells by tumor necrosis factor a, interleukin-2, lipopolysaccharide or phorbol myristic acetate, nor in human melanoma cell line SB-2 by UV irradiation, under conditions which induced the homologue CXC intercrine IL-8 expression. Furthermore, there was no induction of hIRH gene expression, but rather a suppression, upon serum or cytokine addition to serum-deprived fibroblast cell lines, to an in vitro mouse bone marrow preparation, and to monocytic cell line THP-1.

L21 ANSWER 3 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1999:310927 SCISEARCH
THE GENUINE ARTICLE: 187GQ
TITLE: CXCR4 **mRNA** expression in colon, esophageal and gastric **cancers** and hepatitis C infected liver
AUTHOR: Mitra P; Shibuta K; Mathai J; Shimoda K; Banner B F; Mori M; Barnard G F (Reprint)
CORPORATE SOURCE: UNIV MASSACHUSETTS, MED CTR, DIV DIGEST DIS & NUTR S6 737,
55 LAKE AVE N, WORCESTER, MA 01655 (Reprint); UNIV MASSACHUSETTS, MED CTR, DIV DIGEST DIS & NUTR S6 737, WORCESTER, MA 01655; UNIV MASSACHUSETTS, MED CTR, DEPT PATHOL, WORCESTER, MA 01655; KYUSHU UNIV, MED INST BIOREGULAT, DEPT SURG, BEPPU, OITA, JAPAN
COUNTRY OF AUTHOR: USA; JAPAN
SOURCE: INTERNATIONAL JOURNAL OF ONCOLOGY, (**MAY 1999**)
Vol. 14, No. 5, pp. 917-925.
Publisher: PROFESSOR D A SPANDIDOS, 1, S MERKOURI ST, EDITORIAL OFFICE, ATHENS 116 35, GREECE.
ISSN: 1019-6439.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English

REFERENCE COUNT: 49

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We have recently demonstrated by Northern blot and RT-PCR that the mRNA expression of the alpha-chemokine hIRH/SDF-1 alpha is reduced in hepatocellular carcinoma (HCC), several digestive tract cancers and premalignant colon adenomas, and that its receptor CXCR4 mRNA expression is reduced in HCC. Here we investigate the expression of CXCR3 mRNA expression in several digestive tract cancers and hepatitis C viral (HCV) infected liver, a premalignant condition. There was no difference in the CXCR4 mRNA expression in colon, esophageal or gastric cancers compared to non-cancerous tissues. This is significantly different from the reduced expression we have seen with hepatocellular carcinoma ($p<0.05$). To better refine regional tumor or hepatic cytokine mRNA analysis within a biopsy sample we describe a micro-isolation technique for RNA extraction from portal and triad areas of liver biopsies of other small malignant or non-malignant biopsy samples suitable for use in RT-PCR and differential display reactions. In HCV liver biopsies, the expression of hIRH and its receptor CXCR4 mRNA, corrected for G3PDH, was not significantly different from that of control non-HCV (steatosis) biopsies. CXCR3 is expressed on leukocytes and its expression was predicted to correlate with hepatic inflammation. CXCR4 receptor mRNA expression did correlate significantly with that of its ligand hIRH/SDF-1 alpha ($p=0.001$), and with the severity of fibrosis ($p<0.05$), but not with portal inflammation ($p<0.10$), piecemeal necrosis ($p<0.10$), lobular inflammation ($p>0.10$), the presence of lymphoid aggregates ($p>0.10$), or the total histological activity index ($p=0.07$). There was no difference in expression of hIRH or CXCR3 between responders and non-responders to interferon (IFN) treatment, while as a control, the responder group of patients did show a higher expression of IFN alpha receptor than the non-responder group ($p=0.05$).

L21 ANSWER 4 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1999:62142 SCISEARCH
THE GENUINE ARTICLE: 155BH
TITLE: **mRNA** differential display of 2-amino-1-methyl-6-phenylinlidazo[4,5-b]pyridine-induced rat mammary gland **tumors**
AUTHOR: RobertsThomson S J; Snyderwine E G (Reprint)
CORPORATE SOURCE: NCI, CHEM CARCINOGENESIS SECT, EXPT CARCINOGENESIS LAB, DIV BASIC SCI, BLDG 37, ROOM 3C28, BETHESDA, MD 20892 (Reprint); NCI, CHEM CARCINOGENESIS SECT, EXPT CARCINOGENESIS LAB, DIV BASIC SCI, BETHESDA, MD 20892; UNIV QUEENSLAND, SCH PHARM, BRISBANE, QLD, AUSTRALIA
COUNTRY OF AUTHOR: USA; AUSTRALIA
SOURCE: BREAST CANCER RESEARCH AND TREATMENT, (**SEP 1998**) Vol. 51, No. 2, pp. 99-107. Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS. ISSN: 0167-6806.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 49

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The mRNA differential display technique was used to compare mRNAs between normal mammary gland and turner-derived epithelial cells from

female Sprague-Dawley rat mammary gland tumors induced by the heterocyclic amine 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine (PhIP) and promoted by a high-fat diet (23.5% corn oil). Two genes, beta-casein and transferrin, were identified as differentially expressed. The expression of these genes was examined across a bank of rat mammary gland tumors derived from animals on a low-fat diet (5% corn oil) or the high-fat diet.

Carcinomas had over a 10- and 50-fold lower expression of beta-casein and transferrin, respectively than normal mammary gland. In addition, carcinomas from animals on the high-fat diet showed on average a 5-fold higher expression of beta-casein, and transferrin than carcinomas from animals on the low-fat diet. The results indicate the process of mammary gland tumorigenesis alters the expression of certain genes in the mammary gland, and that the level of dietary fat further modulates the expression of these genes.

L21 ANSWER 5 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1998:660816 SCISEARCH
THE GENUINE ARTICLE: 113GY
TITLE: Messenger **RNA** differential display reverse-transcriptase-polymerase-chain-reaction analysis of a progestogen-suppressive gene in a human endometrial-**cancer** cell line
AUTHOR: Sakata M (Reprint); Kurachi H; Morishige K; Ogura K; Yamaguchi M; Nishio Y; Ikegami H; Miyake A; Murata Y
CORPORATE SOURCE: OSAKA UNIV, SCH MED, DEPT OBSTET & GYNECOL, 2-2 YAMADAOKA, SUITA, OSAKA 565, JAPAN (Reprint)
COUNTRY OF AUTHOR: JAPAN
SOURCE: INTERNATIONAL JOURNAL OF CANCER, (**25 SEP 1998**) Vol. 78, No. 1, pp. 125-129. Publisher: WILEY-LISS, DIV JOHN WILEY & SONS INC, 605 THIRD AVE, NEW YORK, NY 10158-0012. ISSN: 0020-7136.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 25

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Progestogen suppresses the progression of endometrial cancer and has an important effect on the secretory change of human endometrium. We characterized the progestogen-induced alterations of gene expression in a human endometrial-cancer cell line using a mRNA differential-display reverse-transcriptase-polymerase-chain-reaction (DDRT-PCR) method. After 5-day incubation of Ishikawa endometrial-cancer cells, with or without 100 nM meduoxyprogesterone acetate (MPA), total RNA was isolated from confluent cells. We identified 8 candidate genes by mRNA differential display by screening up to approximately 3,000 mRNA species. Among these, 2 genes named T21A and T21B showed a decrease in mRNA by MPA treatment when analyzed by Northern blot. Nucleotide sequence showed that clone T21A was part of human mitochondrial shore-chain enoyl-CoA hydratase cDNA. The other clone, T21B, showed no homology with any known nucleotide sequences.

Northern-blot analysis using T21A and T21B clones as probes showed a

decrease in mRNA in human endometrium from the luteal stage, with high serum estradiol and progesterone levels, as compared with that from the early follicular stage, with low serum estradiol and progesterone levels, and that from the pre-ovulatory stage with high serum estradiol and low progesterone levels. These findings suggest that mRNA DDRT-PCR could be used to identify the candidate genes regulated by progestogen in human endometrial cancer and in normal human endometrium. (C) 1998 Wiley-Liss, Inc.

L21 ANSWER 6 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1998:340997 SCISEARCH
THE GENUINE ARTICLE: ZK485
TITLE: Identification of a differential expression of two **cDNAs** between malignant **mesothelioma** and normal mesothelial cells using the **RNA** fingerprint method
AUTHOR: Frank S (Reprint); vonSpecht B U; Sendt W; Farthmann E H; Hirsch T
CORPORATE SOURCE: UNIV FREIBURG, DEPT GEN SURG, HUGSTETTER STR 55, D-79106 FREIBURG, GERMANY (Reprint)
COUNTRY OF AUTHOR: GERMANY
SOURCE: TUMOR BIOLOGY, (**MAY-JUN 1998**) Vol. 19, No. 3, pp. 153-159.
Publisher: KARGER, ALLSCHWILERSTRASSE 10, CH-4009 BASEL, SWITZERLAND.
ISSN: 1010-4283.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 22

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The RNA fingerprint method was used to identify mRNAs that were differentially expressed during the development of human mesothelial cell cancer, We report the isolation of two differentially expressed clones, One clone was expressed in the metastatic mesothelioma cell line M1A and in the malignant mesothelioma cell line M1 and downregulated in normal mesothelial cells, M1 and M1A were derived from a primary and metastatic tumor of the same patient, The other clone was only expressed in normal mesothelial cells, The different expression pattern was confirmed by Northern blot analysis, One clone had a striking sequence homology to the soares pregnant uterus NbHPU homo sapiens cDNA clone, The other clone contained a high sequence homology to the human mRNA for ORF, The biological function of the corresponding genes is unknown, The specificity of expression of the two sequence tags was further examined on different cancer cell lines and normal tissues.

L21 ANSWER 7 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1998:235081 SCISEARCH
THE GENUINE ARTICLE: ZB892
TITLE: Reduced lysyl oxidase messenger **RNA** levels in experimental and human prostate **cancer**
AUTHOR: Ren C Z; Yang G; Timme T L; Wheeler T M; Thompson T C (Reprint)
CORPORATE SOURCE: BAYLOR COLL MED, SCOTT DEPT UROL, 6560 FANNIN, SUITE 2100, HOUSTON, TX 77030 (Reprint); BAYLOR COLL MED, SCOTT DEPT UROL, HOUSTON, TX 77030; BAYLOR COLL MED, DEPT PATHOL,

HOUSTON, TX 77030; BAYLOR COLL MED, DEPT CELL BIOL, HOUSTON, TX 77030; BAYLOR COLL MED, DEPT RADIOL, HOUSTON, TX 77030

COUNTRY OF AUTHOR: USA

SOURCE: CANCER RESEARCH, (**15 MAR 1998**) Vol. 58, No. 6, pp. 1285-1290.
Publisher: AMER ASSOC CANCER RESEARCH, PO BOX 11806, BIRMINGHAM, AL 35202.
ISSN: 0008-5472.

DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 27

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB To identify genes associated with prostate cancer progression, we developed a strategy involving the use of differential display PCR and a panel of genetically matched primary tumor-and metastasis-derived mouse prostate cancer cell Lines, We analyzed sequences that were differentially stimulated by transforming growth factor-beta 1 in primary tumor-versus metastasis-derived cell lines, based on our previous studies indicating that acquisition of differential responses to this growth factor could result in phenotypic traits that facilitate tumor metastasis from specific cell clones within the primary tumor. Using this system, we isolated and sequenced a cDNA fragment that encoded mouse lysyl oxidase (LO) and was induced by transforming growth factor-beta 1d in primary tumor but not in metastasis-derived cells, Northern blotting analysis revealed increased LO expression in a panel of primary tumor cell lines but significantly reduced or nondetectable expression in their matched metastatic counterparts, Further in situ hybridization analysis revealed LO expression in normal mouse prostate epithelium but, in most cases, progressive loss of expression in primary prostate cancer and associated metastatic lesions, Importantly, in situ hybridization studies of normal human prostate and prostate malignancies revealed a similar loss of expression during progression to metastasis, The progressive loss of LO expression during prostate cancer progression provides information that may increase our understanding of the mechanisms that underlie this disease, In addition, LO may provide a useful molecular marker and/or establish a novel therapeutic target for prostate cancer.

L21 ANSWER 8 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)

ACCESSION NUMBER: 97:435194 SCISEARCH
THE GENUINE ARTICLE: XC009

TITLE: Expression of a novel **mRNA** in human head and neck squamous cell **carcinoma** cells

AUTHOR: Werner J A (Reprint); Gorogh T; Lippert B M; Gottschlich S; Heidorn K; Folz B J; Rudert H

CORPORATE SOURCE: CHRISTIAN ALBRECHTS UNIV KIEL, DEPT OTORHINOLARYNGOL HEAD & NECK SURG, ARNOLD HELLER STR 14, D-24105 KIEL, GERMANY (Reprint); CHRISTIAN ALBRECHTS UNIV KIEL, DEPT HEMATOPATHOL, D-24098 KIEL, GERMANY

COUNTRY OF AUTHOR: GERMANY

SOURCE: JOURNAL OF CLINICAL PATHOLOGY-MOLECULAR PATHOLOGY, (**APR 1997**) Vol. 50, No. 2, pp. 82-86.
Publisher: BRITISH MED JOURNAL PUBL GROUP, BRITISH MED ASSOC HOUSE, TAVISTOCK SQUARE, LONDON, ENGLAND WC1H 9JR.

ISSN: 1355-2910.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 33

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Aims-The differential display reverse transcription polymerase chain reaction (DDRT-PCR) technique was used to search for differences between the mRNA expression profiles of squamous cell carcinoma (SCC) cell lines established from head and neck tumours and normal keratinocytes from the mucosa of the upper aerodigestive tract.

Methods-Total RNA prepared from both cell types was reverse transcribed into cDNA then amplified in a PCR mixture. To compare the electrophoretic patterns, mRNAs were amplified by nested PCR using specific oligonucleotides. Additionally, using labelled cDNA probes, northern hybridisation was carried out on three cancer cell lines of different origin, a biopsy from a parotid gland pleomorphic adenoma, healthy mucosa, and keratinocytes.

Results-Comparison of the separated bands revealed a fragment with a differential expression pattern in the SCC cells. This cloned sequence of a 336 base pair mRNA fragment exhibited no significant homology with known transcripts. Additionally, after amplification and sequencing of the 3' end of the fragment no homology with a known human gene sequence was found. However, low homology with a genomic sequence of a nematode was found. Northern hybridisation confirmed the selective expression of this fragment in SCC cells versus the cancer cell lines of different origin, the biopsy of the pleomorphic adenoma, keratinocytes, and healthy mucosa.

Conclusions-This is the first differentially expressed human genome transcript of squamous cell. carcinoma of the head and neck identified by DDRT-PCR. It may prove useful, in the future, to characterise this tumour type.

L21 ANSWER 9 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 97:164686 SCISEARCH
THE GENUINE ARTICLE: WH815
TITLE: Identification of a breast **cancer**-specific gene, BCSG1, by direct differential **cDNA** sequencing
AUTHOR: Ji H J; Liu Y L E; Jia T L; Wang M S; Liu J W; Xiao G W; Joseph B K; Rosen C; Shi Y E (Reprint)
CORPORATE SOURCE: ALBERT EINSTEIN COLL MED, LONG ISL JEWISH MED CTR, SCHNEIDER CHILDRENS HOSP, PEDIAT RES CTR, NEW HYDE PK, NY 11042 (Reprint); ALBERT EINSTEIN COLL MED, LONG ISL JEWISH MED CTR, SCHNEIDER CHILDRENS HOSP, PEDIAT RES CTR, NEW HYDE PK, NY 11042; ALBERT EINSTEIN COLL MED, LONG ISL JEWISH MED CTR, SCHNEIDER CHILDRENS HOSP, PEDIAT RES CTR, NEW HYDE PK, NY 11042; HUMAN GENOME SCI INC, ROCKVILLE, MD 20850; MT STATES MED RES INST, BOISE, ID 83702; DEPT VET AFFAIRS MED CTR, BOISE, ID 83702
COUNTRY OF AUTHOR: USA
SOURCE: CANCER RESEARCH, (**15 FEB 1997**) Vol. 57, No. 4, pp. 759-764.
Publisher: AMER ASSOC CANCER RESEARCH, PUBLIC LEDGER BLDG,

SUITE 816, 150 S. INDEPENDENCE MALL W., PHILADELPHIA, PA 19106.
ISSN: 0008-5472.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 49

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A high-throughput direct-differential cDNA sequencing approach was employed to identify genes differentially expressed in normal breast as compared with breast cancer, Approximately 6000 expressed sequence tags (ESTs) from cDNA libraries of normal breast and breast carcinoma were selected randomly and subjected to EST-sequencing analysis, The relative expression levels of more than 2000 unique EST groups were quantitatively compared in normal versus cancerous breast, Of many putative differentially expressed genes, a breast cancer-specific gene, BCSG1, which was expressed in high abundance in a breast cancer cDNA library but scarcely in a normal breast cDNA library, was identified as a putative breast cancer marker, In situ hybridization analysis demonstrated stage-specific BCSG1 expression as follows: BCSG1 was undetectable in normal or benign breast lesions, showed partial expression in ductal carcinoma in situ, but was expressed at an extremely high level in advanced infiltrating breast cancer, The predicted amino acid sequence of BCSG1 gene has a significant sequence homology to the non-amyloid beta protein fragment of the Alzheimer's disease amyloid protein, BCSG1 overexpression may indicate breast cancer malignant progression from benign breast or in situ carcinoma to the highly infiltrating carcinoma.

L21 ANSWER 10 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 96:866614 SCISEARCH
THE GENUINE ARTICLE: VT536
TITLE: Increased expression of T-plastin gene in cisplatin-resistant human **cancer** cells: Identification by **mRNA** differential display
AUTHOR: Hisano T; Ono M; Nakayama M; Naito S; Kuwano M; Wada M (Reprint)
CORPORATE SOURCE: KYUSHU UNIV, SCH MED, DEPT BIOCHEM, FUKUOKA 81282, JAPAN (Reprint); KYUSHU UNIV, SCH MED, DEPT BIOCHEM, FUKUOKA 81282, JAPAN; KYUSHU UNIV, SCH MED, DEPT UROL, FUKUOKA 81282, JAPAN
COUNTRY OF AUTHOR: JAPAN
SOURCE: FEBS LETTERS, (**11 NOV 1996**) Vol. 397, No. 1, pp. 101-107.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0014-5793.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 51

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The cellular resistance to the potent anticancer agent cis-diamminedichloroplatinum(II) (cisplatin) is thought to be mediated by multiple mechanisms. The technique of differential display of mRNAs was applied to various cisplatin-resistant cell lines and the corresponding parental sensitive human bladder, prostatic, and head and neck cancer cells in order to identify genes that underlie cisplatin resistance. Twenty-four clones were confirmed by Northern blot analysis to be

expressed differentially between resistant and the corresponding sensitive cells. Partial DNA sequences of the eight clones that showed a threefold or greater increase in expression in either the resistant cells (seven clones) or sensitive cells (one clone) revealed that two mere derived from the T-plastin gene and one from the tissue factor gene. The abundance of T-plastin mRNA in cisplatin-resistant T24/DDP10 cell was similar to 12 times that in the parental T24 cells. Transfection of T24/DDP10 cells with a vector encoding full-length T-plastin antisense RNA demonstrated that reduced T-plastin expression was associated with increased sensitivity to cisplatin. These results are consistent with the hypothesis that several mechanisms participate cooperatively in the acquisition of cisplatin resistance in human cancer.

L21 ANSWER 11 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 96:553812 SCISEARCH
THE GENUINE ARTICLE: UY063
TITLE: IDENTIFICATION BY DIFFERENTIAL DISPLAY OF A MESSENGER-**RNA** SPECIFICALLY INDUCED BY 12-O-TETRADECANOYLPHORBOL-13-ACETATE (TPA) IN T84 HUMAN COLON-**CARCINOMA** CELLS
AUTHOR: CAFFERATA E G; GONZALEZGUERRICO A M; PIVETTA O H; SANTACOLOMA T A (Reprint)
CORPORATE SOURCE: FDN CAMPOMAR, INST INVEST BIOQUIM, AV PATRICIAS ARGENTINAS 435, RA-1405 BUENOS AIRES, DF, ARGENTINA (Reprint); FDN CAMPOMAR, INST INVEST BIOQUIM, RA-1405 BUENOS AIRES, DF, ARGENTINA; INST NACL GENET MED, BUENOS AIRES, DF, ARGENTINA
COUNTRY OF AUTHOR: ARGENTINA
SOURCE: CELLULAR AND MOLECULAR BIOLOGY, (**JUL 1996**) Vol. 42, No. 5, pp. 797-804.
ISSN: 0145-5680.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 16

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB 12-o-Tetradecanoylphorbol-13-Acetate (TPA) down-regulates the expression of the gene responsible for cystic fibrosis (CFTR). To understand the mechanism by which TPA down-regulates CFTR, we decided to study genes specifically induced by this phorbol ester in T84 human colon carcinoma cells, which highly express CFTR, using differential display. Several strategies that allowed us to overcome false-positive reactions in differential displays are described. We have detected different cDNAs obtained from mRNAs specifically induced by TPA. A cDNA fragment corresponding to a mRNA of approximately 2.2 kb was sequenced. Part of this sequence has been reported by others in GenBank and corresponds to a cDNA from a human lung library. The function is unknown and does not have any significant homology with other sequences. It is expressed after two hrs in T84 cells treated with TPA, reaching a maximum response by four hrs. The dose-response curve shows increased mRNA levels starting at 10 ng/ml of TPA and reaching a maximum by 50 ng/ml TPA (10-fold stimulation over control). This mRNA shows a rapid and large response to TPA and it might be involved in the differentiation of T84 cells induced by TPA.

L21 ANSWER 12 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 96:552791 SCISEARCH
THE GENUINE ARTICLE: UY023
TITLE: IDENTIFICATION OF MESSENGER-**RNAS** DIFFERENTIALLY EXPRESSED IN QUIESCENCE OR IN LATE G1 PHASE OF THE CELL-CYCLE IN HUMAN BREAST-**CANCER** CELLS BY USING THE DIFFERENTIAL DISPLAY METHOD
AUTHOR: ALPAN R S; SPARVERO S; PARDEE A B (Reprint)
CORPORATE SOURCE: HARVARD UNIV, SCH MED, DANA FARBER CANC INST D810, DIV CELL GROWTH & REGULAT, 44 BINNEY ST, BOSTON, MA, 02115 (Reprint); HARVARD UNIV, SCH MED, DANA FARBER CANC INST D810, DIV CELL GROWTH & REGULAT, BOSTON, MA, 02115; HARVARD UNIV, SCH MED, DEPT BIOL CHEM & MOLEC PHARMACOL, BOSTON, MA, 02115
COUNTRY OF AUTHOR: USA
SOURCE: MOLECULAR MEDICINE, (**JUL 1996**) Vol. 2, No. 4, pp. 469-478.
ISSN: 1076-1551.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: ENGLISH
REFERENCE COUNT: 23

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Background: The decision for a cell to enter the DNA synthesis (S) phase of the cell cycle or to arrest in quiescence is likely to be determined by genes expressed in the late G1 phase, at the restriction point. Loss of restriction point control is associated with malignant cellular transformation and cancer. For this reason, identifying genes that are differentially expressed in late G1 phase versus quiescence is important for understanding the molecular basis of normal and malignant growth.

Materials and Methods: The differential display (DD) method detects mRNA species that are different between sets of mammalian cells, allowing their recovery and cloning of the corresponding cDNAs. Using this technique, we compared mRNAs from synchronized human breast cancer cells (21PT) in quiescence and in late G1.

Results: Six mRNAs differentially expressed in lace G1 or in quiescence were identified. One mRNA expressed 10 hr after serum induction showed 99% homology to a peptide transporter involved in antigen presentation of the class I major histocompatibility complex (TAP-1) mRNA. Another mRNA expressed specifically in quiescence and down-regulated 2 hr following serum induction showed 98% homology to human NADP(+)-dependent cytoplasmic malic enzyme (EC1.1.1.40) mRNA, which is an important enzyme in fatty add synthesis and lipogenesis. Three others showed high homology to different mRNAs in the GeneBank, corresponding to genes having unknown functions. Finally, one mRNA revealed no significant homology to known genes in the GeneBank.

Conclusions: We conclude that DD is an efficient and powerful method for the identification of growth-related genes which may have a role in cancer development.

L21 ANSWER 13 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:846741 SCISEARCH
THE GENUINE ARTICLE: TH623

TITLE: IDENTIFICATION OF A TRANSPOSON-RELATED **RNA** DOWN-REGULATED BY RETINOIC ACID IN EMBRYONAL **CARCINOMA** AND EMBRYONIC STEM-CELLS
AUTHOR: HIROSE T; AUSTIN S J; JETTEN A M (Reprint)
CORPORATE SOURCE: NIEHS, CELL BIOL SECT, PULM PATHOBIOL LAB, RES TRIANGLE PK, NC, 27709 (Reprint); NIEHS, CELL BIOL SECT, PULM PATHOBIOL LAB, RES TRIANGLE PK, NC, 27709
COUNTRY OF AUTHOR: USA
SOURCE: EXPERIMENTAL CELL RESEARCH, (**DEC 1995**) Vol. 221, No. 2, pp. 294-300.
ISSN: 0014-4827.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 41

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The differential display polymerase chain reaction was employed to identify changes in mRNA expression during retinoic acid-induced differentiation in embryonal carcinoma PCC4.aza1R cells, In this study, we report on one cDNA, EC1, that was identified by this method, EC-1 encodes a 0.6-kb mRNA that is present in PCC4.aza1R cells and down-regulated by retinoic acid, Sequence analysis revealed that EC-1 exhibits a 47% identity with the early transposon RNA ETn and does not contain a long open reading frame, EC-1 mRNA expression was reduced by 50% after 24 h of treatment with 10 nM retinoic acid and was undetectable after 48 h, Down-regulation of EC-1 mRNA was observed at retinoic acid concentrations as low as 0.1 nM. EC-1 was found to be expressed in several other embryonal carcinoma cell lines as well as in embryonic stem cells but was undetectable in differentiated cell types obtained after RA treatment, Northern blot analysis using RNA from multiple mouse tissues demonstrated that the expression of EC-1 is restricted to the testis, Treatment of PCC4.aza1R cells with an RAR-selective agonist also repressed the expression of EC-1 mRNA while treatment with an RXR-selective agonist reduced EC-1 expression slightly. The RAR alpha-specific antagonist Ro 41-5253 had little effect on the downregulation of EC-1 by retinoic acid, Our observations indicate that the repression of EC-1 is associated with the induction of differentiation in embryonal carcinoma and embryonic stem cells and involves an RAR-activated signaling pathway. (C) 1995 Academic Press, Inc.

L21 ANSWER 14 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:745156 SCISEARCH
THE GENUINE ARTICLE: RU338
TITLE: IDENTIFICATION OF DIFFERENTIALLY EXPRESSED MESSENGER-**RNAS** DURING NEURONAL DIFFERENTIATION OF P19 EMBRYONAL **CARCINOMA**-CELLS
AUTHOR: SUZUKI Y (Reprint); WANAKA A; TOHYAMA M; TAKAGI T
CORPORATE SOURCE: OSAKA UNIV, SCH MED, DEPT MOLEC NEUROBIOL TANABE, 2-2 YAMADAOKA, SUITA, OSAKA 565, JAPAN (Reprint); OSAKA UNIV, SCH MED, DEPT ANAT & NEUROSCI, SUITA, OSAKA 565, JAPAN
COUNTRY OF AUTHOR: JAPAN
SOURCE: NEUROSCIENCE RESEARCH, (**AUG 1995**) Vol. 23, No. 1, pp. 65-71.
ISSN: 0168-0102.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE

LANGUAGE: ENGLISH
REFERENCE COUNT: 22
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB To understand the basic mechanisms underlying neuronal differentiation, we have attempted to isolate differentially expressed genes, which may play a key role in this complex process, from neuronal differentiating P19 embryonal carcinoma cells. RNA fingerprinting by the arbitrarily primed PCR (RAP) method was adapted to detect such differentially expressed genes during P19 neuronal differentiation. Using this method with some modifications, we successfully cloned seven cDNA fragments which were expressed differentially within the first 48 h after 1 mu M retinoic acid (RA) treatment, which ultimately induces neuronal differentiation. Comparison of the partial nucleotide sequences of these clones with sequences in DNA databases indicated that one of these clones was identical to a region of the mouse Oct-3 gene, which has been shown to be dramatically repressed by RA. Two clones were highly homologous to the human profilinII and leucine-rich protein genes. The other four clones were not closely related to any sequences in the databases. Except for the Oct-3 gene, the other six genes isolated here have not been reported previously as RA-regulated genes. RAP is, thus, a promising method for identification of novel and potentially important genes which are differentially regulated during neuronal differentiation.

L21 ANSWER 15 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:486111 SCISEARCH
THE GENUINE ARTICLE: RH966
TITLE: **RNA** GENETICS OF BREAST-**CANCER** - MASPIN AS PARADIGM
AUTHOR: SAGER R (Reprint); SHENG S; ANISOWICZ A; SOTIROPOULOU G; ZOU Z; STENMAN G; SWISSHELM K; CHEN Z; HENDRIX M J C; PEMBERTON P; RAFIDI K; RYAN K
CORPORATE SOURCE: DANA FARBER CANC INST, BOSTON, MA, 02115 (Reprint); GOTHENBURG UNIV, SAHLGRENSKA HOSP, DEPT PATHOL, CANC GENET LAB, S-41345 GOTHENBURG, SWEDEN; UNIV WASHINGTON, DEPT PATHOL, SEATTLE, WA, 98195; ST LOUIS UNIV, CARDINAL GLENNON CHILDRENS HOSP, SCH MED, PEDIAT RES INST, ST LOUIS, MO, 63110; LXR BIOTECHNOL INC, RICHMOND, CA, 94804
COUNTRY OF AUTHOR: USA; SWEDEN
SOURCE: COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY, (**1994**) Vol. 59, pp. 537-546.
ISSN: 0091-7451.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 40

L21 ANSWER 16 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:301868 SCISEARCH
THE GENUINE ARTICLE: QU879
TITLE: ISOLATION OF **CDNAS** THAT ARE DIFFERENTIALLY EXPRESSED BETWEEN ANDROGEN-DEPENDENT AND ANDROGEN-INDEPENDENT PROSTATE **CARCINOMA**-CELLS USING DIFFERENTIAL DISPLAY PCR

AUTHOR: BLOK L J; KUMAR M V; TINDALL D J (Reprint)
CORPORATE SOURCE: MAYO CLIN & MAYO FDN, DEPT UROL RES, 17 GUGGENHEIM, ROCHESTER, MN, 55905 (Reprint); MAYO CLIN & MAYO FDN, DEPT UROL RES, ROCHESTER, MN, 55905; MAYO CLIN & MAYO FDN, DEPT BIOCHEM MOLEC BIOL, ROCHESTER, MN, 55905
COUNTRY OF AUTHOR: USA
SOURCE: PROSTATE, (**APR 1995**) Vol. 26, No. 4, pp. 213-224

ISSN: 0270-4137.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 43

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In the development of prostate cancer there is an important transition from androgen-dependent growth (which can be treated) to androgen-independent growth (which is beyond medical control). This transition is probably accompanied by genetic changes, resulting in the activation of oncogenes or the inactivation of tumor suppressor genes. In the present manuscript, the isolation of genes that may be involved in advanced, androgen-independent prostate cancer growth is described.

Using differential display PCR, 13 cDNAs were isolated representing genes that are differentially expressed between the androgen-dependent prostate carcinoma cell line LNCaP and the androgen-independent prostate carcinoma cell lines PC-3 and DU 145. These clones were divided into four groups: androgen-responsive genes (TL5, TL25, TL32, and TL35); genes with a marked decreased expression in one of the prostate cancer cell lines (TL27); genes with a marked, increased expression in one or more of the prostate cancer cell lines (TL4, TL16, TL21, and TL22); and genes with minor (but repeatable) changes in expression between prostate cancer cell lines (TL7, TL15, TL18, and TL33). The 13 genes were analyzed for their sequence information, tissue specificity, and androgen responsiveness in order to identify genes of interest.

In summary, differential display PCR appears to provide an attractive alternative to existing molecular techniques to screen for differentially expressed genes in prostate cancer cells. (C) 1995 Wiley-Liss, Inc.

L21 ANSWER 17 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:209191 SCISEARCH
THE GENUINE ARTICLE: QM109
TITLE: IDENTIFICATION AND PARTIAL SEQUENCE OF A **CDNA** THAT IS DIFFERENTIALLY EXPRESSED IN HUMAN BRAIN-**TUMORS**
AUTHOR: SHINOURA N; SHAMRAJ O I; HUGENHOLZ H; ZHU J G; MCBLACK P; WARNICK R; TEW J J; WANI M A; MENON A G (Reprint)
CORPORATE SOURCE: UNIV CINCINNATI, COLL MED, DEPT MOLEC GENET BIOCHEM & MICROBIOL, 231 BETHESDA AVE, CINCINNATI, OH, 45267 (Reprint); UNIV CINCINNATI, COLL MED, DEPT MOLEC GENET BIOCHEM & MICROBIOL, CINCINNATI, OH, 45267; OTTAWA GEN HOSP, DEPT NEUROSURG, OTTAWA, ON K1H 8L6, CANADA; HARVARD UNIV, BRIGHAM & WOMENS HOSP, SCH MED, DEPT NEUROSURG, BOSTON, MA, 02114; UNIV CINCINNATI, COLL MED, DEPT NEUROSURG, CINCINNATI, OH, 45267
COUNTRY OF AUTHOR: USA; CANADA
SOURCE: CANCER LETTERS, (**02 MAR 1995**) Vol. 89, No. 2, pp. 215-221.

ISSN: 0304-3835.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 14

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Differential display technique was used to identify mRNAs that are differentially expressed in malignant versus benign brain tumors. Using this method, a novel 1.4-kb long cDNA (MM1) clone was isolated and sequenced. The nucleotide and the translated amino acid sequence of MM1 cDNA clone did not show significant homology to any known sequence in the Genebank. The expression of MM1 appears to be almost eightfold higher in glioblastomas compared to low grade astrocytomas and slightly higher in malignant meningiomas than in benign meningiomas. The size of mRNA from northern analysis appears to be 7 kb, which is much higher than the size of the isolated MM1 cDNA clone. Expression of MM1 was also seen in various cell lines derived from human tumors including glioblastomas. Whereas low level expression was seen in kidney, esophagus, liver, lymph node, ovary and testis, none of the other tissues from a total of 18 different human organs showed any MM1 expression.

L21 ANSWER 18 OF 18 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 93:496221 SCISEARCH
THE GENUINE ARTICLE: LR606
TITLE: IDENTIFICATION OF DIFFERENTIALLY EXPRESSED **RNA** IN HUMAN OVARIAN-**CARCINOMA** CELLS BY ARBITRARILY PRIMED PCR FINGERPRINTING OF TOTAL **RNAS**
AUTHOR: WONG K K; MOK C H (Reprint); WELSH J T; MCCLELLAND M; TSAO S W; BERKOWITZ R S
CORPORATE SOURCE: BRIGHAM & WOMENS HOSP, DEPT OBSTET GYNECOL & REPROD BIOL, GYNECOL ONCOL LAB, BOSTON, MA, 02115; CALIF INST BIOL RES, LA JOLLA, CA, 92037
COUNTRY OF AUTHOR: USA
SOURCE: INTERNATIONAL JOURNAL OF ONCOLOGY, (**JUL 1993**) Vol. 3, No. 1, pp. 13-17.
ISSN: 1019-6439.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 22

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Using arbitrarily primed PCR fingerprinting of RNA (RAP), we have analyzed RNAs prepared from two normal ovarian surface epithelial cell cultures, two normal mesothelial cell cultures, and eight independent ovarian carcinoma cell lines. Each arbitrarily chosen primer gave a unique fingerprint of about 30 cDNA products. Most of the cDNA products produced by any particular primer were shared between all cell lines. However, one primer detected a cDNA PCR product that was absent in all eight ovarian carcinoma cell lines but present in all normal cell cultures. We have cloned and sequenced the DNA fragment that distinguishes normal from ovarian carcinoma cell lines. The DNA sequence has one continuous open reading frame throughout which indicates that it may be from a translated gene. Furthermore, we confirmed the differential expression of the gene by

Northern blot analysis. We also observed that the intensity of the band in the RNA fingerprint correlates with the expression level of the corresponding RNA. These results further demonstrate the ability of RAP to detect differentially expressed genes in a quantitative manner and demonstrated the application of RAP for the detection of differential gene expression during carcinogenesis.

=>

L1 ANSWER 1 OF 1 MEDLINE
ACCESSION NUMBER: 93092151 MEDLINE
DOCUMENT NUMBER: 93092151 PubMed ID: 1458489
TITLE: Differential display and cloning of messenger RNAs from human breast cancer versus mammary epithelial cells.
AUTHOR: Liang P; Averboukh L; Keyomarsi K; Sager R; Pardee A B
CORPORATE SOURCE: Division of Cell Growth and Regulation, Dana-Farber Cancer Institute, Boston, Massachusetts 02115.
CONTRACT NUMBER: GM 24571 (NIGMS)
SOURCE: CANCER RESEARCH, **(1992 Dec 15) 52** (24) **6966-8.**
Journal code: CNF; 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-S50179; GENBANK-S50182; GENBANK-S50184; GENBANK-S50185; GENBANK-S72766; GENBANK-S72767; GENBANK-S72768; GENBANK-S72769; GENBANK-S72771; GENBANK-X63098
ENTRY MONTH: 199301
ENTRY DATE: Entered STN: 19930129
Last Updated on STN: 19930129
Entered Medline: 19930108

AB Identification of the genes that are specifically expressed in tumor cells but not in normal cells (oncogenes), or vice versa (tumor suppressor genes), is important for understanding the molecular basis of cancer. The differential display technique was applied to compare mRNAs from normal and tumor-derived human mammary epithelial cells, cultured under the same conditions. Complementary DNA fragments corresponding to several apparently differentially expressed mRNAs were recovered and sequenced. They exhibit characteristics of the 3' end of eukaryotic mRNA, as predicted by the method. A complementary DNA fragment seen only in the normal cell was used as a probe to isolate its corresponding complementary DNA clone from a library. Northern analysis confirmed its differential expression. Thus, this method can be used for detecting, cloning, and sequencing of genes that are unique to a host of biological and disease processes.

=> file scisearch

L20 ANSWER 3 OF 6 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1998389283 MEDLINE
DOCUMENT NUMBER: 98389283 PubMed ID: 9723890
TITLE: Identification of a second **stanniocalcin** cDNA in mouse and human: **stanniocalcin** 2.
AUTHOR: **Chang A C; Reddel R R**
CORPORATE SOURCE: Children's Medical Research Institute, Sydney, NSW, Australia.
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, **(1998 Jun 25)** 141 (1-2) 95-9.
Journal code: E69; 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF055460; GENBANK-AF056244
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981112

AB It has recently been shown that mammals contain a gene encoding a protein that is related to **stanniocalcin** (STC), a hormone previously considered to be present only in bony fish where it plays a major role in Ca2+ homeostasis. Here we report the identification in the mouse and human of a cDNA, STC-2, that shows significant similarity to the first mammalian STC (which we now rename STC-1). Northern analysis revealed that mammalian STC-2, like STC-1, is expressed in a wide variety of tissues. In contrast to STC-1, the predicted amino acid sequence of STC-2 contains a cluster of histidine residues in the C-terminal portion of the protein, which suggests that STC-2 may interact with metal ions.

L20 ANSWER 4 OF 6 MEDLINE DUPLICATE 4

L7 ANSWER 4 OF 9 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1999145369 MEDLINE
DOCUMENT NUMBER: 99145369 PubMed ID: 10022771
TITLE: Molecular cloning and characterization of **stanniocalcin**-related protein.
AUTHOR: DiMattia G E; Varghese R; Wagner G F
CORPORATE SOURCE: Department of Oncology, The University of Western Ontario, The London Regional Cancer Centre, Canada..
dimattia@julian.uwo.ca
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, **(1998 Nov 25)** 146 (1-2) 137-40.
Journal code: E69; 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990517
Last Updated on STN: 19990517
Entered Medline: 19990503

AB **Stanniocalcin** (STC) is a glycoprotein hormone first discovered in fish and recently identified in humans and mice. In this report we have described the cloning of an STC-like cDNA, designated here as STC related protein (STCrP). Human STCrP (hSTCrP) cDNAs were isolated as expressed sequence tags (ESTs) and predicted a polypeptide of 302 amino acids, with 58%, homology to human STC (hSTC). Ten of the eleven 1/2 cysteine residues that in STC allow for dimerization of monomeric subunits were conserved in hSTCrP. By Northern analysis, three hSTCrP mRNAs were detected and were most abundant in pancreas, spleen and kidney as well as a variety of different transformed cell lines. The high degree of sequence homology suggests that STC and STCrP may have been derived from a common ancestral gene.

L10 ANSWER 15 OF 19 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:250622 CAPLUS
DOCUMENT NUMBER: 133:133356
TITLE: Assessment of Stanniocalcin-1 mRNA as a molecular marker for micrometastases of various human **cancers**
AUTHOR(S): Fujiwara, Yoshiyuki; Sugita, Yurika; Nakamori, Shoji; Miyamoto, Atsushi; Shiozaki, Ken; Nagano, Hiroaki; Sakon, Masato; Monden, Morito
CORPORATE SOURCE: Department of Surgery and Clinical Oncology, Osaka University, Osaka, 565-0871, Japan
SOURCE: Int. J. Oncol. (2000), 16(4), 799-804
CODEN: IJONES; ISSN: 1019-6439
PUBLISHER: International Journal of Oncology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We assessed Stanniocalcin-1 (STC-1) mRNA expression in human normal tissues, various types of human **cancer** cell lines, and **cancer** tissues obtained during surgery. Using a reverse transcriptase-polymerase chain reaction (RT-PCR) assay developed to detect STC-1 mRNA, the transcripts were detected in 20 out of 21 **cancer** cell lines and in all **tumor** tissues from various types of **cancer**. Semi-quant. analyses with multiplex RT-PCR showed that STC-1 mRNA tended to be enhanced in **cancer** tissues of hepatocellular **carcinoma** and colorectal **cancer** compared to background **cancer**-free tissues. Anal. of blood samples obtained from 11 patients with hepatocellular **carcinoma** before, after and during hepatectomy showed STC-1 mRNA expression in 8 out of 11 patients at least one time. Normal donor blood samples (n=31) were all-neg. for STC-1 mRNA expression. Our results indicate that STC-1 mRNA might be a useful mol. marker for detection of **tumor** cells in blood from patients with various types of **malignancies**.
REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 16 OF 19 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:19480 CAPLUS
DOCUMENT NUMBER: 132:74509
TITLE: A method and a kit for diagnosing leukemia using stanniocalcin as a **tumor** marker
INVENTOR(S): Koide, Yoshio; Igarashi, Akira; Fu, Jianguo; Takano, Shouichi; Sasaki, Takeshi
PATENT ASSIGNEE(S): BML K. K., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 10 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000002709	A2	20000107	JP 1998-181503	19980613

AB A convenient method is provided for accurately diagnosing leukemia using stanniocalcin as a **tumor** marker. Stanniocalcin is a glycoprotein specifically recognized in blood of a patient upon developing leukemia. More specifically, stanniocalcin is recognized in the blood cell fraction from which red blood cells are excluded. The occurrence of stanniocalcin is examd. either by an immunol. method using antibodies to stanniocalcin or by a genetic amplification method detecting mRNA for stanniocalcin in the blood cell fraction. A test kit including at least antibodies to stanniocalcin protein or heat-stable DNA polymerase for diagnosing leukemia is claimed. MRNA for stanniocalcin was detected with most of leukemia patients, but not with healthy persons at all. Stanniocalcin protein was detected with leukemia cells by flow cytometry using anti-stanniocalcin monoclonal antibody.

L10 ANSWER 17 OF 19 CAPLUS COPYRIGHT 2002 ACS

L12 ANSWER 4 OF 5 JAPIO COPYRIGHT 2002 JPO
ACCESSION NUMBER: 2000-002709 JAPIO
TITLE: LEUKEMIA DETECTING METHOD AND DETECTION KIT
INVENTOR: KOIDE YOSHIO; IGARASHI AKIRA; KO TAKEKUNI; TAKANO SHOICHI; SASAKI TAKESHI
PATENT ASSIGNEE(S): BML:KK)
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 2000002709A		20000107	Heisei	G01N033-68

JP
APPLICATION INFORMATION
ST19N FORMAT: JP1998-181503 19980613
ORIGINAL: JP10181503 Heisei
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined Applications, Vol. 2000

AN 2000-002709 JAPIO
AB PROBLEM TO BE SOLVED: To find out a specific factor detected in a body fluid specimen when a person contracts leukemia, and to provide a simple and accurate diagnostic method for the leukemia using this specific factor as the base.
SOLUTION: A state of **stanniocalcin** of a blood corpuscle fraction of blood, preferably a blood corpuscle fraction from which a red blood corpuscle fraction is removed is grasped by a detection method using an antigen-antibody reaction between an antibody to the **stanniocalcin** and the **stanniocalcin**, detection of mRNA of the **stanniocalcin** in the blood corpuscle fraction, or the like. Using the **stanniocalcin** as an index of the leukemia diagnosis can make the diagnosis method simple and accurate.

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L14: Entry 1 of 2 File: JPAB Jan 7, 2000

PUB-NO: JP02000002709A
DOCUMENT-IDENTIFIER: JP 2000002709 A
TITLE: LEUKEMIA DETECTING METHOD AND DETECTION KIT

PUBN-DATE: January 7, 2000

INVENTOR-INFORMATION:

NAME	COUNTRY
KOIDE, YOSHIO	
IGARASHI, AKIRA	
KO, TAKEKUNI	
TAKANO, SHOICHI	
SASAKI, TAKESHI	

ASSIGNEE-INFORMATION:

NAME	COUNTRY
BML:KK	

APPL-NO: JP10181503
APPL-DATE: June 13, 1998

INT-CL (IPC): G01N 33/68; C12N 15/02; G01N 33/53; C12P 21/08

ABSTRACT:

PROBLEM TO BE SOLVED: To find out a specific factor detected in a body fluid specimen when a person contracts leukemia, and to provide a simple and accurate diagnostic method for the leukemia using this specific factor as the base.

SOLUTION: A state of stanniocalcin of a blood corpuscle fraction of blood, preferably a blood corpuscle fraction from which a red blood corpuscle fraction is removed is grasped by a detection method using an antigen-antibody reaction between an antibody to the stanniocalcin and the stanniocalcin, detection of mRNA of the stanniocalcin in the blood corpuscle fraction, or the like. Using the stanniocalcin as an index of the leukemia diagnosis can make the diagnosis method simple and accurate.

WEST

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L14: Entry 2 of 2 File: DWPI Jan 7, 2000

DERWENT-ACC-NO: 2000-131570
DERWENT-WEEK: 200016

TITLE: Diagnosis of leukemia - involves evaluating stanniocalcin present in leucocytes using antibody specific for stanniocalcin

PATENT-ASSIGNEE: BML KK (BMLBN)

PRIORITY-DATA: 1998JP-0181503 (June 13, 1998)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
JP 2000002709 A	January 7, 2000		009	G01N033/68

APPLICATION-DATA:

PUB-NO	APPL-DATE	APPL-NO	DESCRIPTOR
JP2000002709A	June 13, 1998	1998JP-0181503	

INT-CL (IPC): C12N 15/02; C12P 21/08; G01N 33/53; G01N 33/68

ABSTRACTED-PUB-NO: JP2000002709A
BASIC-ABSTRACT:

NOVELTY - Diagnosis of leukemia comprising evaluating the presence of stanniocalcin in leucocytes using a specific antibody, is new. Stanniocalcin present in the blood cell fraction, excluding erythrocyte, is evaluated for diagnosing leukemia. DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for leukemia diagnosis kit comprising antibody specific for stanniocalcin protein and heat resistant DNA-polymerase.

USE - The method is useful for diagnosing leukemia.

ADVANTAGE - The diagnosis method is simple and specific.

ABSTRACTED-PUB-NO: JP2000002709A
EQUIVALENT-ABSTRACTS:

CHOSEN-DRAWING: Dwg.0/1

DERWENT-CLASS: B04 D16 S03
CPI-CODES: B04-B04D; B04-G01; B04-L04A; B11-C07A; B11-C08E3; B11-C08E5; B12-K04A1; B12-K04F; D05-H09; D05-H11; D05-H14B;
EPI-CODES: S03-E14H; S03-E14H4;

L22 ANSWER 1 OF 11 BIOTECHDS COPYRIGHT 2002 DERWENT INFORMATION LTD
ACCESSION NUMBER: 2001-10582 BIOTECHDS
TITLE: Novel assay for diagnosing and monitoring cancer, involves determining levels of **Lng108** in cells, tissues or bodily fluids of the patient, and comparing with control; vaccine
AUTHOR: Recipon H; Macina R A; Chen S Y; Sun Y
PATENT ASSIGNEE: Diadexus
LOCATION: Santa Clara, CA, USA.
PATENT INFO: WO 2001032209 10 May 2001
APPLICATION INFO: WO 2000-US30482 3 Nov 2000
PRIORITY INFO: US 1999-163444 4 Nov 1999
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2001-316386 [33]
AN 2001-10582 BIOTECHDS
AB Diagnosing the presence of cancer or diagnosis of metastases of cancer in
a patient, involves determining levels of **Lng108** in a sample (S1) of cells, tissues, or bodily fluids in a patient and comparing the determined levels with levels of **Lng108** in sample (S2) of cells, tissues or body fluids from a normal human control. Also claimed are: staging cancer in a patient; monitoring cancer in a patient for the onset of metastasis; monitoring a change in stage of cancer in a patient;
identifying potential therapeutic agent for use in imaging and treating cancer; imaging cancer in a patient by administering an antibody specific
for **Lng108**; and a vaccine for treating cancer, by immunogenically stimulating the amount of **Lng108**. (36pp)

L28 ANSWER 1 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 97:267781 SCISEARCH
THE GENUINE ARTICLE: WQ548
TITLE: Mob-1, a Ras target gene, is overexpressed in colorectal cancer
AUTHOR: Zhang R; Zhang H; Zhu W M; **Pardee A B**; Coffey R J; **Liang P (Reprint)**
CORPORATE SOURCE: VANDERBILT UNIV, DEPT CELL BIOL, SCH MED, VANDERBILT CANC CTR, NASHVILLE, TN 37232 (Reprint); VANDERBILT UNIV, DEPT CELL BIOL, SCH MED, VANDERBILT CANC CTR, NASHVILLE, TN 37232; VANDERBILT UNIV, DEPT MED & CELL BIOL, NASHVILLE, TN 37232; VANDERBILT UNIV, VET AFFAIRS MED CTR, NASHVILLE, TN 37232; DANA FARBER CANC INST, DIV CELL GROWTH & REGULAT, BOSTON, MA 02115
COUNTRY OF AUTHOR: USA
SOURCE: ONCOGENE, (**3 APR 1997**) Vol. 14, No. 13, pp. 1607-1610.
Publisher: STOCKTON PRESS, HOUNDMILLS, BASINGSTOKE, HAMPSHIRE, ENGLAND RG21 6XS.
ISSN: 0950-9232.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 17

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Mutations in the ras oncogenes have been linked to many different cancers, In contrast to the extensive body of knowledge related to the genetics of ras activation, relatively little is known of the transcriptional events triggered by ras, In previous work we have used differential display to identify Mob-1, a member of alpha-chemokine family, as one of the immediate transcriptional targets following Ras activation, Here, we provide additional experimental evidence to support this finding by the use of an inducible H-ras expression system, the treatment of Ras farnesyl transferase inhibitor and activation of endogenous Ras by serum growth factors, We further demonstrate that IP-10, the human homolog of Mob-1, is overexpressed in the majority of colorectal cancers.

L28 ANSWER 2 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 96:552791 SCISEARCH
THE GENUINE ARTICLE: UY023
TITLE: IDENTIFICATION OF MESSENGER-RNAS DIFFERENTIALLY EXPRESSED IN QUIESCENCE OR IN LATE G1 PHASE OF THE CELL-CYCLE IN HUMAN BREAST-CANCER CELLS BY USING THE DIFFERENTIAL DISPLAY METHOD
AUTHOR: ALPAN R S; SPARVERO S; **PARDEE A B (Reprint)**
CORPORATE SOURCE: HARVARD UNIV, SCH MED, DANA FARBER CANC INST D810, DIV CELL GROWTH & REGULAT, 44 BINNEY ST, BOSTON, MA, 02115 (Reprint); HARVARD UNIV, SCH MED, DANA FARBER CANC INST D810, DIV CELL GROWTH & REGULAT, BOSTON, MA, 02115; HARVARD UNIV, SCH MED, DEPT BIOL CHEM & MOLEC PHARMACOL, BOSTON, MA, 02115
COUNTRY OF AUTHOR: USA
SOURCE: MOLECULAR MEDICINE, (**JUL 1996**) Vol. 2, No. 4,

pp. 469-478.
ISSN: 1076-1551.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: ENGLISH
REFERENCE COUNT: 23

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Background: The decision for a cell to enter the DNA synthesis (S) phase of the cell cycle or to arrest in quiescence is likely to be determined by genes expressed in the late G1 phase, at the restriction point. Loss of restriction point control is associated with malignant cellular transformation and cancer. For this reason, identifying genes that are differentially expressed in late G1 phase versus quiescence is important for understanding the molecular basis of normal and malignant growth.

Materials and Methods: The differential display (DD) method detects mRNA species that are different between sets of mammalian cells, allowing their recovery and cloning of the corresponding cDNAs. Using this technique, we compared mRNAs from synchronized human breast cancer cells (21PT) in quiescence and in late G1.

Results: Six mRNAs differentially expressed in lace G1 or in quiescence were identified. One mRNA expressed 10 hr after serum induction showed 99% homology to a peptide transporter involved in antigen presentation of the class I major histocompatibility complex (TAP-1) mRNA. Another mRNA expressed specifically in quiescence and down-regulated 2 hr following serum induction showed 98% homology to human NADP(+)-dependent cytoplasmic malic enzyme (EC1.1.1.40) mRNA, which is an important enzyme in fatty add synthesis and lipogenesis. Three others showed high homology to different mRNAs in the GeneBank, corresponding to genes having unknown functions. Finally, one mRNA revealed no significant homology to known genes in the GeneBank.

Conclusions: We conclude that DD is an efficient and powerful method for the identification of growth-related genes which may have a role in cancer development.

L28 ANSWER 3 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 96:370736 SCISEARCH
THE GENUINE ARTICLE: UJ638
TITLE: BETTER GEL RESOLUTION AND LONGER CDNAS INCREASE THE PRECISION OF DIFFERENTIAL DISPLAY
AUTHOR: **AVERBOUKH L (Reprint)**; DOUGLAS S A; ZHAO S; LOWE K; MAHER J; **PARDEE A B**
CORPORATE SOURCE: CHILDRENS HOSP, DANA FARBER CANC INST, DIV CELL GROWTH & REGULAT, 44 BINNEY ST, BOSTON, MA, 02115 (Reprint); SMITHKLINE BEECHAM PHARMACEUT, KING OF PRUSSIA, PA, 19406;
GENOMYX, FOSTER CITY, CA, 00000
COUNTRY OF AUTHOR: USA
SOURCE: BIOTECHNIQUES, (**MAY 1996**) Vol. 20, No. 5, pp. 918-921.
ISSN: 0736-6205.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 6

L28 ANSWER 4 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:799539 SCISEARCH
THE GENUINE ARTICLE: BE08E
TITLE: ANALYSIS OF ALTERED GENE-EXPRESSION BY DIFFERENTIAL DISPLAY
AUTHOR: **LIANG P (Reprint)**; BAUER D; **AVERBOUKH L**; WARTHOE P; ROHRWILD M; MULLER H; STRAUSS M; **PARDEE A B**
CORPORATE SOURCE: DANA FARBER CANC INST, DIV CELL GROWTH & REGULAT, BOSTON, MA, 02115 (Reprint); HUMBOLDT UNIV BERLIN, MAX DELBRUCK CTR MOLEC MED, MAX PLANCK SOC, D-13122 BERLIN, GERMANY; HARVARD UNIV, SCH MED, DEPT CELL BIOL, BOSTON, MA, 02115; DANISH CANC SOC, DIV CANC BIOL, DK-2100 COPENHAGEN, DENMARK
COUNTRY OF AUTHOR: USA; GERMANY; DENMARK
SOURCE: METHODS IN ENZYMOLOGY, (**1995**) Vol. 254, pp. 304-321.
ISSN: 0076-6879.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 22

L28 ANSWER 5 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:486111 SCISEARCH
THE GENUINE ARTICLE: RH966
TITLE: RNA GENETICS OF BREAST-CANCER - MASPIN AS PARADIGM
AUTHOR: **SAGER R (Reprint)**; SHENG S; ANISOWICZ A; SOTIROPOULOU G; ZOU Z; STENMAN G; SWISSHELM K; CHEN Z; HENDRIX M J C; PEMBERTON P; RAFIDI K; RYAN K
CORPORATE SOURCE: DANA FARBER CANC INST, BOSTON, MA, 02115 (Reprint); GOTHENBURG UNIV, SAHLGRENSKA HOSP, DEPT PATHOL, CANC GENET LAB, S-41345 GOTHENBURG, SWEDEN; UNIV WASHINGTON, DEPT PATHOL, SEATTLE, WA, 98195; ST LOUIS UNIV, CARDINAL GLENNON CHILDRENS HOSP, SCH MED, PEDIAT RES INST, ST LOUIS, MO, 63110; LXR BIOTECHNOL INC, RICHMOND, CA, 94804
COUNTRY OF AUTHOR: USA; SWEDEN
SOURCE: COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY, (**1994**) Vol. 59, pp. 537-546.
ISSN: 0091-7451.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 40

L28 ANSWER 6 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:343641 SCISEARCH
THE GENUINE ARTICLE: QX634
TITLE: RECENT ADVANCES IN DIFFERENTIAL DISPLAY
AUTHOR: **LIANG P (Reprint)**; **PARDEE A B**
CORPORATE SOURCE: DANA FARBER CANC INST, DIV CELL GROWTH & REGULAT, 44 BINNEY ST, BOSTON, MA, 02115 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: CURRENT OPINION IN IMMUNOLOGY, (**APR 1995**) Vol. 7, No. 2, pp. 274-280.
ISSN: 0952-7915.

DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 41
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Differential display and RNA arbitrary primed polmerase chain reaction are methods recently designed to identify and isolate differentially expressed genes. Methodological modifications have since been introduced to streamline the techniques. The major effort has centered on how to eliminate false positives as approached from a variety of angles, ranging from RNA sample preparation, northern blot confirmation, primer length variation, to better experimental design.

L28 ANSWER 7 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 94:405703 SCISEARCH
THE GENUINE ARTICLE: NV420
TITLE: CHRONIC CARDIAC REJECTION - IDENTIFICATION OF 5 UP-REGULATED GENES IN TRANSPLANTED HEARTS BY DIFFERENTIAL MESSENGER-RNA DISPLAY
AUTHOR: UTANS U; **LIANG P**; WYNER L R; KARNOVSKY M J; RUSSELL M E (Reprint)
CORPORATE SOURCE: HARVARD UNIV, SCH PUBL HLTH, CARDIOVASC BIOL LAB, 677 HUNTINGTON AVE, BOSTON, MA, 02115 (Reprint); HARVARD UNIV, SCH PUBL HLTH, CARDIOVASC BIOL LAB, BOSTON, MA, 02115; HARVARD UNIV, SCH MED, BOSTON, MA, 02115; BRIGHAM & WOMENS HOSP, DIV CARDIOVASC, BOSTON, MA, 02115
COUNTRY OF AUTHOR: USA
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (**05 JUL 1994**) Vol. 91, No. 14, pp. 6463-6467.
ISSN: 0027-8424.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 21
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Transplant arteriosclerosis, the major manifestation of chronic rejection, develops after allogeneic (Lewis to F344) but not syngeneic (Lewis to Lewis) rat cardiac transplantation. To identify transcriptionally regulated mediators associated with chronic cardiac rejection, we adapted the differential mRNA display technique for in vivo transplant specimens. Gene transcript patterns in four allogeneic hearts showing early signs of chronic rejection were compared with those in two syngeneic hearts exposed to the same surgical procedure but histologically normal. Twelve differentially expressed cDNA bands were identified. We improved the probability of isolating one or more allograft-specific cDNAs from a single display band by first using recovered and reamplified PCR products as probes in RNA blot analysis. cDNA fragments cloned from individual bands were then used ire a second RNA blot analysis, which allowed for the correlation of specific mRNA transcripts with cDNA clones.

Five cDNA clones produced time dependent, allograft-specific hybridization. Sequence analysis demonstrated that two of these cDNAs corresponded to unknown genes, whereas the other three represented known

genes not previously associated with chronic rejection. The latter group included the macrophage lectin specific for galactose/N-acetylgalactosamine (a cell-surface receptor), the nuclear P1 gene (a homologue of a yeast replication protein), and a ubiquitin-like gene. Our application of the differential display technique allowed the direct identification of potential mediators under in vivo conditions that preserve the environment of the disease process-including infiltrating cell populations critical to the inflammatory response.

L28 ANSWER 8 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 94:367687 SCISEARCH
THE GENUINE ARTICLE: NP970
TITLE: A CAUTIONARY NOTE ON REACTION TUBES FOR DIFFERENTIAL DISPLAY AND CDNA AMPLIFICATION IN THERMAL CYCLING
AUTHOR: CHEN Z H (Reprint); SWISSHELM K; **SAGER R**
CORPORATE SOURCE: HARVARD UNIV, SCH MED, DANA FARBER CANC INST, DIV CANC GENET, 44 BINNEY ST, BOSTON, MA, 02115 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: BIOTECHNIQUES, (**JUN 1994**) Vol. 16, No. 6, pp. 1002.
ISSN: 0736-6205.
DOCUMENT TYPE: Note; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 5

L28 ANSWER 9 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 94:50852 SCISEARCH
THE GENUINE ARTICLE: MT966
TITLE: MASPIN, A SERPIN WITH TUMOR-SUPPRESSING ACTIVITY IN HUMAN MAMMARY EPITHELIAL-CELLS
AUTHOR: ZOU Z Q; ANISOWICZ A; HENDRIX M J C; THOR A; NEVEU M; SHENG S J; RAFIDI K; SEFTOR E; **SAGER R (Reprint)**
CORPORATE SOURCE: HARVARD UNIV, SCH MED, DANA FARBER CANC INST, DIV CANC GENET, 44 BINNEY ST, BOSTON, MA, 02115 (Reprint); HARVARD UNIV, SCH MED, DANA FARBER CANC INST, DIV CANC GENET, 44 BINNEY ST, BOSTON, MA, 02115; UNIV ARIZONA, CTR CANC, TUCSON, AZ, 85724; MASSACHUSETTS GEN HOSP, DEPT PATHOL, BOSTON, MA, 02114
COUNTRY OF AUTHOR: USA
SOURCE: SCIENCE, (**28 JAN 1994**) Vol. 263, No. 5146, pp. 526-529.
ISSN: 0036-8075.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: PHYS; LIFE; AGRI
LANGUAGE: ENGLISH
REFERENCE COUNT: 21

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A gene encoding a protein related to the serpin family of protease inhibitors was identified as a candidate tumor suppressor gene that may play a role in human breast cancer. The gene product, called maspin, is expressed in normal mammary epithelial cells but not in most mammary carcinoma cell lines. Transfection of MDA-MB-435 mammary carcinoma cells with the maspin gene did not alter the cells' growth properties in vitro, but reduced the cells' ability to induce tumors and metastasize in nude mice and to invade through a basement membrane matrix in vitro. Analysis of human breast cancer specimens revealed that loss of maspin expression occurred most frequently in advanced cancers. These results support the

hypothesis that maspin functions as a tumor suppressor.

L28 ANSWER 10 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 93:482472 SCISEARCH
THE GENUINE ARTICLE: LQ337
TITLE: IDENTIFICATION BY DIFFERENTIAL DISPLAY OF ALPHA-6 INTEGRIN
AS A CANDIDATE TUMOR-SUPPRESSOR GENE
AUTHOR: **SAGER R (Reprint)**; ANISOWICZ A; NEVEU M; **LIANG P**; SOTIROPOULOU G
CORPORATE SOURCE: HARVARD UNIV, SCH MED, DANA FARBER CANC INST, DIV CANC GENET, 44 BINNEY ST, BOSTON, MA, 02115 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: FASEB JOURNAL, (**JUL 1993**) Vol. 7, No. 10, pp. 964-970.
ISSN: 0892-6638.
DOCUMENT TYPE: Note; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 33
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A new method of differential expression cloning called differential display (DD) has been used to screen for novel tumor suppressor genes involved in breast cancer. The screen is based on positive selection at the mRNA level for genes expressed in normal mammary epithelial cells but decreased or lost in corresponding tumor cells. A candidate tumor suppressor gene recovered by DD is integrin alpha-6 (alpha6), a component of the heterodimeric integrin receptors alpha6beta1 and alpha6beta4. Loss of alpha6 expression was confirmed in total RNAs by Northern blot analysis and by immunostaining with alpha6 antibodies. Consistent with these cell culture findings, previous immunostaining of mammary tissue sections has identified decreased alpha6 protein expression during breast tumor progression. Southern blot analysis demonstrated that alpha6 gene is present in tumor cell lines, suggesting that re-expression may be inducible by pharmacological intervention. The likelihood that alpha6 may have tumor suppressing activity is supported by growing evidence of a central role for integrins in transducing growth control and differentiation signals from growth factors and the extracellular matrix (ECM).

L28 ANSWER 11 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 93:461507 SCISEARCH
THE GENUINE ARTICLE: LN960
TITLE: DISTRIBUTION AND CLONING OF EUKARYOTIC MESSENGER-RNAS BY MEANS OF DIFFERENTIAL DISPLAY - REFINEMENTS AND OPTIMIZATION
AUTHOR: **LIANG P (Reprint)**; **AVERBOUKH L**; **PARDEE A B**
CORPORATE SOURCE: HARVARD UNIV, SCH MED, DANA FARBER CANC INST, DIV CELL GROWTH & REGULAT, BOSTON, MA, 02115 (Reprint); HARVARD UNIV, SCH MED, DEPT BIOL CHEM & MOLEC PHARMACOL, BOSTON, MA, 02115
COUNTRY OF AUTHOR: USA
SOURCE: NUCLEIC ACIDS RESEARCH, (**11 JUL 1993**) Vol. 21, No. 14, pp. 3269-3275.
ISSN: 0305-1048.
DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 16

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Differential display has been developed as a tool to detect and characterize altered gene expression in eukaryotic cells. The basic principle is to systematically amplify messenger RNAs and then distribute their 3' termini on a denaturing polyacrylamide gel. Here we provide methodological details and examine in depth the specificity, sensitivity and reproducibility of the method. We show that the number of anchored oligo-dT primers can be reduced from twelve to four that are degenerate at the penultimate base from the 3' end. We also demonstrate that using optimized conditions described here, multiple RNA samples from related cells can be displayed simultaneously. Therefore process-specific rather than cell-specific genes could be more accurately identified. These results enable further streamlining of the technique and make it readily applicable to a broad spectrum of biological systems.

=>

L10 ANSWER 19 OF 19 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:403247 CAPLUS
DOCUMENT NUMBER: 125:83287
TITLE: Genetic changes during immortalization of human cells
AUTHOR(S): Reddel, Roger R.; Bryan, Tracy M.; Rogan, Eileen M.; Noble, Jane R.; Maclean, Kenneth; Whitaker, Noel J.; Chang, Andy C.-M.
CORPORATE SOURCE: Children's Medical Research Institute, Westmead, 2145, Australia
SOURCE: Radiat. Oncol. Invest. (1996), Volume Date 1995-1996, 3(6), 299-306
CODEN: ROINEU; ISSN: 1065-7541
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Spontaneous immortalization of fibroblasts contg. an inherited mutation of one p53 allele was assocd. with loss of the wild-type p53 allele and loss of p16INK4 gene expression, but this combination of genetic events was insufficient for immortalization. Loss of p16INK4 expression appears to be an alternative to loss of functional retinoblastoma gene product. In all cell lines studied, immortalization was assocd. either with stabilization of telomere length in the presence of telomerase activity or with the acquisition of long and heterogeneous telomeres in the absence of detectable telomerase. The role of other genes, such as human stanniocalcin, in the immortalization process is under investigation.

L7 ANSWER 3 OF 9 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1998372535 MEDLINE
DOCUMENT NUMBER: 98372535 PubMed ID: 9708804
TITLE: High expression of **stanniocalcin** in differentiated brain neurons.
AUTHOR: Zhang K Z; Westberg J A; Paetau A; von Boguslawsky K; Lindsberg P; Erlander M; Guo H; Su J; Olsen H S; Andersson L C
CORPORATE SOURCE: Department of Pathology, Haartman Institute, University of Helsinki, Finland.
SOURCE: AMERICAN JOURNAL OF PATHOLOGY, **(1998 Aug)** 153 (2) 439-45.
Journal code: 3RS; 0370502. ISSN: 0002-9440.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980903
Last Updated on STN: 19980903
Entered Medline: 19980825

AB **Stanniocalcin** (STC) is a glycoprotein hormone first found in fish, in which it regulates calcium homeostasis and protects against hypercalcemia. Human and mouse stc cDNA were recently cloned. We found a dramatically upregulated expression of STC during induced neural differentiation in a human neural crest-derived cell line, Paju. Immunohistochemical staining of sections from human and adult mouse brain revealed abundant presence of STC in the neurons with no activity in the glial cells. STC expression was not seen in immature brain neurons of fetal or newborn mice. Given that STC has been found to regulate calcium/phosphate metabolism in some mammalian epithelia, we suggest that STC may act as a regulator of calcium homeostasis in terminally differentiated brain neurons.

L7 ANSWER 4 OF 9 MEDLINE DUPLICATE 3

L16 ANSWER 5 OF 15 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1999145369 MEDLINE
DOCUMENT NUMBER: 99145369 PubMed ID: 10022771
TITLE: Molecular cloning and characterization of **stanniocalcin**-related protein.
AUTHOR: DiMattia G E; Varghese R; Wagner G F
CORPORATE SOURCE: Department of Oncology, The University of Western Ontario, The London Regional Cancer Centre, Canada.. dimattia@julian.uwo.ca
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, **(1998 Nov 25)** 146 (1-2) 137-40.
Journal code: 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990517
Last Updated on STN: 19990517
Entered Medline: 19990503

AB **Stanniocalcin** (STC) is a glycoprotein hormone first discovered in fish and recently identified in humans and mice. In this report we have described the cloning of an STC-like cDNA, designated here as STC related protein (STCrP). Human STCrP (hSTCrP) cDNAs were isolated as expressed sequence tags (ESTs) and predicted a polypeptide of 302 amino acids, with 58%, homology to human STC (hSTC). Ten of the eleven 1/2 cysteine residues that in STC allow for dimerization of monomeric subunits were conserved in hSTCrP. By Northern analysis, three hSTCrP mRNAs were detected and were most abundant in pancreas, spleen and kidney as well as a variety of different transformed cell lines. The high degree of sequence homology suggests that STC and STCrP may have been derived from a common ancestral gene.

L16 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:403247 CAPLUS
DOCUMENT NUMBER: 125:83287
TITLE: Genetic changes during immortalization of human cells
AUTHOR(S): Reddel, Roger R.; Bryan, Tracy M.; Rogan, Eileen M.; Noble, Jane R.; Maclean, Kenneth; Whitaker, Noel J.; Chang, Andy C.-M.
CORPORATE SOURCE: Children's Medical Research Institute, Westmead, 2145, Australia
SOURCE: Radiation Oncology Investigations (**1996**), Volume Date 1995-1996, 3(6), 299-306
CODEN: ROINEU; ISSN: 1065-7541
PUBLISHER: Wiley-Liss
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Spontaneous immortalization of fibroblasts contg. an inherited mutation of one p53 allele was assocd. with loss of the wild-type p53 allele and loss of p16INK4 gene expression, but this combination of genetic events was insufficient for immortalization. Loss of p16INK4 expression appears to be an alternative to loss of functional retinoblastoma gene product. In all cell lines studied, immortalization was assocd. either with stabilization of telomere length in the presence of telomerase activity or with the acquisition of long and heterogeneous telomeres in the absence of detectable telomerase. The role of other genes, such as human **stanniocalcin**, in the immortalization process is under investigation.

L16 ANSWER 11 OF 15 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 95:55329 SCISEARCH
THE GENUINE ARTICLE: QA375
TITLE: A HUMAN ORPHAN CALCITONIN RECEPTOR-LIKE STRUCTURE
AUTHOR: FLUHMANN B; MUFF R; HUNZIKER W; FISCHER J A; BORN W (Reprint)
CORPORATE SOURCE: UNIV ZURICH, DEPT ORTHOPAED SURG, CALCIUM METAB RES LAB, FORCHSTR 340, CH-8008 ZURICH, SWITZERLAND (Reprint); UNIV ZURICH, DEPT ORTHOPAED SURG, CALCIUM METAB RES LAB, CH-8008 ZURICH, SWITZERLAND; UNIV ZURICH, DEPT MED, CH-8008 ZURICH, SWITZERLAND; F HOFFMANN LA ROCHE & CO LTD, CH-4002 BASEL, SWITZERLAND
COUNTRY OF AUTHOR: SWITZERLAND
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (**05 JAN 1995**) Vol. 206, No. 1, pp. 341-347.
ISSN: 0006-291X.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 16

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A novel calcitonin receptor-like protein of 461 amino acids with seven putative transmembrane domains has been identified through molecular cloning in a cDNA library of the human cerebellum. 91% and 56% of the amino acids are identical in a rat orphan calcitonin receptor-like sequence and the human calcitonin receptor, respectively. 5.2 kb mRNA is predominantly expressed in the lung, heart and kidney. Specific binding of I-125-labeled salmon calcitonin and human calcitonin gene-related peptide-I to COS-7 cells transiently transfected with the receptor cDNA was less then 0.5%. Cellular cAMP accumulation was indistinguishable in cDNA transfected and non-transfected control COS-7 and renal tubular cells from the American opossum stimulated with human and salmon calcitonin, human calcitonin gene-related peptide-I and -II, human amylin, human adrenomedullin, lizard helodermin, salmon **stanniocalcin** and chicken parathyroid hormone-related protein. The receptor-like protein whose ligand remains to be discovered belongs to the family of receptors of calcitonin, parathyroid hormone, secretin, vasointestinal peptide and pituitary adenylate cyclase-activating polypeptide. (C) 1995 Academic Press, Inc.

L16 ANSWER 12 OF 15 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 92214238 MEDLINE
DOCUMENT NUMBER: 92214238 PubMed ID: 1666805
TITLE: Salmon **stanniocalcin** and bovine parathyroid hormone have dissimilar actions on mammalian bone.
AUTHOR: Stern P H; Shankar G; Fargher R C; Copp D H; Milliken C E; Sato K J; Goltzman D; Herrmann-Erlee M P
CORPORATE SOURCE: Department of Pharmacology, Northwestern University Medical School, Chicago, IL 60611.
CONTRACT NUMBER: AR 11262 (NIAMS)
SOURCE: JOURNAL OF BONE AND MINERAL RESEARCH, **(1991 Nov)** 6 (11) 1153-9.
Journal code: 8610640. ISSN: 0884-0431.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199205
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Last Updated on STN: 19970203
Entered Medline: 19920504

AB **Stanniocalcin** (STC), a calcium-regulating glycoprotein hormone isolated from the corpuscles of Stannius of salmon, was tested for effects on bone and calcium metabolism in mammalian species (rats and mice). STC generally failed to alter serum calcium of parathyroidectomized rats at concentrations equimolar with effective concentrations of parathyroid hormone (PTH). STC did not increase cAMP in ROS 17/2.8 or UMR-108 osteosarcoma cells, OK kidney cells, fetal rat limb bones, or neonatal mouse calvariae, and similarly failed to increase urinary cAMP in rats. STC did not consistently stimulate resorption in any of the rodent bone culture systems, although variable resorptive responses were elicited in fetal mouse calvariae. The results indicate that this fish hormone has limited, if any, PTH-like activity on calcium metabolism in mammalian systems.

L16 ANSWER 13 OF 15 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 91:615462 SCISEARCH
THE GENUINE ARTICLE: GN465
TITLE: CONTROL OF CALCIUM REGULATING HORMONES IN THE VERTEBRATES - PARATHYROID-HORMONE, CALCITONIN, PROLACTIN, AND **STANNIOCALCIN**
AUTHOR: BONGA S E W (Reprint); PANG P K T
CORPORATE SOURCE: CATHOLIC UNIV NIJMEGEN, FAC SCI, DEPT ANIM PHYSIOL, 6525 ED NIJMEGEN, NETHERLANDS (Reprint); UNIV ALBERTA, SCH MED,
DEPT PHYSIOL, EDMONTON T6G 2H7, ALBERTA, CANADA
COUNTRY OF AUTHOR: NETHERLANDS; CANADA
SOURCE: INTERNATIONAL REVIEW OF CYTOLOGY, (**1991**) Vol. 128, pp. 139-213.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: ENGLISH
REFERENCE COUNT: 334